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(71) Applicant *(for AE, AG, AL, AM, AT, AU, AZ, BA, BB, BE, BF, BG, BJ, BR, BW, BY, BZ, CA, CF, CG, CH, CI, CM, CN, CO, CR, CU, CY, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, FR, GA, GB, GD, GE, GH, GM, GN, GQ, GR, GW, HR, HU, ID, IE, IL, IN, IS, IT, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MC, MD, MK, ML, MN, MR, MW, MX, MZ, NA, NE, NG, NI, NL, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG only)*: **ASTRAZENECA AB** [SE/SE]; SE-151 85 Södertälje (SE).

(71) Applicant *(for MG only)*: **ASTRAZENECA UK LIMITED** [GB/GB]; 15 Stanhope Gate, London Greater London W1K 1LN (GB).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **HUDSON, Kevin** [GB/GB]; AstraZeneca R & D Alderley, Alderley Park, Macclesfield Cheshire SK10 4TG (GB). **SOUTH, Marie, Caroline** [GB/GB]; AstraZeneca R & D Alderley, Alderley Park, Macclesfield Cheshire SK10 4TG (GB). **MARSHALL, Gayle** [GB/GB]; AstraZeneca R & D Alderley, Alderley Park, Macclesfield Cheshire SK10 4TG (GB). **SAM, Mehran** [CA/US]; AstraZeneca R & D Boston, 35 Gatehouse Drive, Waltham, MA 02451 (US).

(74) Agent: **GLOBAL INTELLECTUAL PROPERTY**; AstraZeneca AB, SE-151 85 Södertälje (SE).

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(54) Title: METHOD

(57) Abstract: The invention relates to a method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 or 2 as defined herein whereby to predict an increased likelihood of response to the erbB receptor drug. Preferred genes include any one of NES, GSPT2, ETR101, TAZ, CHST7, DNAJC3, NPAS2, PIN1, TCEA2, VAMP4, DAPK1, DAPK2, MLLT3, TNNC1, KIAA0931, ACOX2, EMP1, SLC20A1, SPRY2 or PGM1.

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METHOD

The present invention relates to sensitivity of tumours to therapeutic agents which can be predicted from the gene expression profile of the tumour and hence that the suitability of cancer patients for treatment with such therapeutic agents can be determined by measuring the relative expression levels of particular genes in tumour tissue.

The phosphorylation of proteins on tyrosine residues is a key element of signal transduction within cells. Enzymes capable of catalysing such reactions are termed tyrosine kinases. A number of these enzymes exist as integral components of transmembrane receptor molecules and are classified as receptor tyrosine kinases (RTKs). There are several members of this family of RTKs, class I of which includes the erbB family, e.g. epidermal growth factor receptor (EGFR), erbB2, erbB3 and erbB4. Binding of a variety of ligands to the external domain activates the EGFR tyrosine kinase domain. Activation causes EGFR itself and a number of cellular substrates to become phosphorylated on tyrosine residues. These phosphorylation reactions are a major component of growth factor induced proliferation of cells.

The erbB family of receptor tyrosine kinases are known to be frequently involved in driving the proliferation and survival of tumour cells (reviewed in Olayioye et al., EMBO J., 2000, 19, 3159). One mechanism by which this can occur is over expression of the receptor at the protein level, for example as a result of gene amplification. This has been observed in many common human cancers (reviewed in Klapper et al., Adv. Cancer Res., 2000, 77, 25) such as, non-small cell lung cancers (NSCLCs) including adenocarcinomas (Cerny et al., Brit. J. Cancer, 1986, 54, 265; Reubi et al., Int. J. Cancer, 1990, 45, 269; Rusch et al., Cancer Research, 1993, 53, 2379; Brabender et al, Clin. Cancer Res., 2001, 7, 1850) as well as other cancers of the lung (Hendler et al., Cancer Cells, 1989, 7, 347.

It is now several decades since the study of retroviral mediated cellular transformation began to revolutionize our understanding of malignant transformation. Transformation was shown to be dependent on oncogenes carried by viruses and these were shown to have mammalian cellular counterparts, proto-oncogenes. In 1984, EGFR was described as the mammalian counterpart of the retroviral oncogene, v-erbB (Downward et al). This, coupled to earlier observations describing a two component autocrine growth promoting mechanism in cancer cells consisting of EGF ligand and its receptor EGFR (Sporn & Todaro), strengthened

the hypothesis that EGFR signalling is an important contributor to tumourigenesis. Subsequent reports continued to provide evidence that EGFR is an attractive target for therapeutic intervention in Cancer (see Yarden & Sliwkowski for review). EGFR is markedly overexpressed across a large variety of epithelial Cancers (see Salomon et al) and some immunohistochemical studies have demonstrated EGFR expression is associated with poor prognosis. In addition to overexpression, it is recognised that there is potential for deregulated EGFR signalling in tumours via a number of alternative mechanisms including i) EGFR mutations ii) increased ligand expression and enhanced autocrine loop and iii) heterodimerisation and cross talk with other erbB receptor family members.

In addition, a wealth of pre-clinical information suggests that the erbB family of receptor tyrosine kinases are involved in cellular transformation. In addition to this, a number of pre-clinical studies have demonstrated that anti-proliferative effects can be induced by knocking out one or more erbB activities by small molecule inhibitors, dominant negatives or inhibitory antibodies (reviewed in Mendelsohn et al., Oncogene, 2000, 19, 6550).

Thus it has been recognised that inhibitors of these receptor tyrosine kinases should be of value as a selective inhibitor of mammalian cancer cells (Yaish et al. Science, 1988, 242, 933, Kolibaba et al, Biochimica et Biophysica Acta, 1997, 133, F217-F248; Al-Obeidi et al, 2000, Oncogene, 19, 5690-5701; Mendelsohn et al, 2000, Oncogene, 19, 6550-6565).

A number of small molecule inhibitors of erbB family of receptor tyrosine kinases are known, particularly inhibitors of EGF and erbB2 receptor tyrosine kinases. For example European Patent Application No. 0566226 and International Patent Applications WO 96/33980 and WO 97/30034 disclose that certain quinazoline derivatives which possess an anilino substituent at the 4-position possess EGFR tyrosine kinase inhibitory activity and are inhibitors of cancer tissue.

It has been disclosed by J R Woodburn et al. in Proc. Amer. Assoc. Cancer Research, 1997, 38, 633 and Pharmacol. Ther., 1999, 82, 241-250 that the compound N-(3-chloro-4-fluorophenyl)-7-methoxy-6-(3-morpholinopropoxy)quinazolin-4-amine is a potent EGFR tyrosine kinase inhibitor. This compound is also known as Iressa (registered trade mark), gefitinib (United States Adopted Name), by way of the code number ZD1839 and Chemical Abstracts Registry Number 184475-35-2. The compound is principally identified hereinafter as gefitinib.

Gefitinib was developed as an inhibitor of epidermal growth factor receptor-tyrosine kinase (EGFR-TK), which blocks signalling pathways responsible for driving proliferation, invasion, and survival of cancer cells (Wakeling, A.E., et al. Cancer Res, 2002, 62(20), p5749). Gefitinib has provided clinical validation of small molecule inhibitors of EGFR. Potent anti-tumour effects as well as rapid improvements in NSCLC-related symptoms and quality of life have been observed in clinical studies that enrolled patients with advanced NSCLC who did not respond to platinum-based chemotherapy. The Phase II 'IDEAL' trials demonstrated that single agent gefitinib resulted in objective anti-tumour activity, symptomatic improvement and limited toxicity in patients with advanced NSCLC and previously treated with cytotoxic chemotherapy (Fukuoka et al., Kris et al). Objective response rate (Complete Response + Partial Response) was 18.4% and 11.8% respectively in the IDEAL 1 and IDEAL 2 trials. The differences in response in these clinical trials has been attributed to different population groups in the two trials, predominantly Japanese in IDEAL 1 and a predominantly European-derived population in IDEAL 2. Beyond objective responses, additional patients experienced stable disease and / or symptom improvement meaning that approximately 50% of patients overall benefit from gefitinib. The tumour response data has been the basis of initial regulatory approvals of gefitinib in advanced NSCLC in several markets.

It is important to be able to understand the basis of response to anti-cancer therapeutic agents such as gefitinib since this would allow clinicians to maximise the benefit/risk ratio for each patient, potentially via the development of diagnostic tests to identify patients most likely to benefit from gefitinib treatment. An obvious candidate marker of response to gefitinib has been EGFR expression level. However, gefitinib inhibition of growth of some cancer-derived cell lines and tumour xenografts is not well correlated with the level of expression of EGFR. Furthermore, studies alongside the IDEAL trials demonstrated that EGFR protein expression as measured by IHC was not an accurate predictor of response to gefitinib (Bailey et al). Although there are now several additional hypotheses based on genetics, genomics, proteomics, biochemical and other studies, there is still no pre-treatment predictive biomarker of gefitinib response currently approved by regulatory authorities. Possibly the most significant recent breakthrough in understanding gefitinib response has come from recent data (Lynch et al, Paez et al) indicating that mutation in the EGFR kinase domain predicts gefitinib hypersensitivity in NSCLC patients. Hypersensitivity is a vague term but in this field is generally understood to mean patients experiencing objective tumour responses (i.e. marked tumour regression,

normally above 50%). As well as demonstrating the EGFR mechanism of action for gefitinib, this may provide a basis for venturing into other disease settings such as first line, adjuvant and possibly earlier cancer intervention with EGFR inhibitors in a targeted subpopulation in NSCLC patients and other types of cancers carrying the EGFR mutation.

However, it is likely that restricting prescription of gefitinib to the mutant EGFR carrying tumour subgroup will deprive many patients who could benefit from gefitinib. Firstly there are emerging reports of gefitinib hypersensitive patients with undetectable EGFR mutation in their tumour and other patients with EGFR mutation who do not respond to gefitinib. Secondly, data reported at ASCO 2004 (Shepherd et al) indicated that the EGFR small molecule tyrosine kinase inhibitor erlotinib (Roche, Genentech, OSI) prolongs survival in advanced NSCLC previously treated with chemotherapy, by ~2 months across the population with resulting 41% reduction in risk of death at one year. Most interestingly, the survival benefit appears to be is derived from patients in the stable disease response population as well as hypersensitive patients. This highlights the likely importance of identifying likely gefitinib responsive patients beyond those carrying EGFR mutation. Definitive survival benefit is also likely to be demonstrated from ongoing clinical trials with gefitinib.

The differential response of patients to chemotherapy treatments indicates that there is a need to find methods of predicting which treatment regimes best suit a particular patient.

There is an increasing body of evidence that suggests that patients' responses to numerous drugs may be related to a patients' genetic, genomic, proteomic, biochemical or profile and that determination of the genetic factors that influence, for example, response to a particular drug could be used to provide a patient with a personalised treatment regime. Such personalised treatment regimes offer the potential to maximise therapeutic benefit to the patient, whilst minimising, for example side effects that may be associated with alternative and less effective treatment regimes.

Therefore there is a need for methods that can predict a patients' response to a drug based on the results of a test that indicates whether the patient is likely to respond to treatment or to be resistant to treatment.

The present invention is based on the discovery that the sensitivity of tumours to therapeutic agents can be predicted from the gene expression profile of the tumour and hence that the suitability of tumour patients for treatment with such therapeutic agents can be determined by measuring the relative expression levels of particular genes in tumour tissue.

According to one aspect of the present invention there is provided a method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 as defined herein whereby to predict an increased likelihood of response to the erbB receptor drug.

According to another aspect of the present invention there is provided a method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 or DAPK2 whereby to predict an increased likelihood of response to the erbB receptor drug.

In one embodiment the method comprises testing a biological sample from the mammal for expression of any one of ACOX2, NPAS2, NES, CHST7, GSPT2, DAPK1, DAPK2 or TNNC1. More preferably the method comprises testing a biological sample from the mammal for expression of any one of NPAS2, NES, CHST7 or DAPK1. More preferably the method comprises testing a biological sample from the mammal for expression of at least two of NPAS2, NES, CHST7 or DAPK1. More preferably the method comprises testing a biological sample from the mammal for expression of at least three of NPAS2, NES, CHST7 or DAPK1. More preferably still the method comprises testing a biological sample from the mammal for expression of NPAS2, NES, CHST7 and DAPK1.

In an alternative embodiment the method comprises testing a biological sample from the mammal for expression of any one of NES, GSPT2, ETR101, TAZ, CHST7, DNAJC3, NPAS2, PIN1, TCEA2, VAMP4, DAPK1, DAPK2, MLLT3, TNNC1 or KIAA0931. More preferably the method comprises testing a biological sample from the mammal for expression of any one of DAPK1, DAPK2 or NES. More preferably the method comprises testing a biological sample from the mammal for expression of at least two of DAPK1, DAPK2 or NES. More preferably the method comprises testing a biological sample from the mammal for expression of DAPK1, DAPK2 and NES.

In a preferred embodiment the method additionally comprises testing a biological sample from the mammal for expression of any gene listed in Table 2 as defined herein. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1, SLC20A1, SPRY2 or PGM1. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

In an alternative preferred embodiment the method additionally comprises testing a biological sample from the mammal for expression of any gene listed in Table 2 as defined herein. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1, HCA127, UBL5, ZNF23, UROD, CD44, SPRY1, RAPGEF2, SLC20A1, NRP1, PGM1, SPRY2, PTGER3, SCN10A, KITLG, CDH1, HOP, BCL3 or OLFM1. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

Preferably the tumour is selected from the group consisting of leukaemia, multiple myeloma, lymphoma, bile duct, bone, bladder, brain, CNS, glioblastoma, breast, colorectal, cervical, endometrial, gastric, head, neck, hepatic, lung, muscle, neuronal, oesophageal, ovarian, pancreatic, pleural membrane, peritoneal membrane, prostate, renal, skin, testicular, thyroid, uterine and vulval. More preferably the tumour is selected from one of non-small cell lung, pancreatic, head or neck. More preferably the tumour is selected from one of non-small cell lung, head or neck.

Preferably the erbB receptor drug is selected from any one of gefitinib, erlotinib, PKI-166, EKB-569, HKI-272, lapatinib, canertinib, AEE788, XL647, BMS 5599626, cetuximab, matuzumab, panitumumab, MR1-1, IMC-11F8 or EGFRL11. Most preferably the erbB receptor drug is gefitinib.

In a further preferred embodiment of the method of the invention the mammal is a human and the method comprises testing a biological sample from the human for increased expression of DAPK1 and decreased expression of NPAS2, NES, CHST7 or EMP1 whereby to predict an increased likelihood of response to gefitinib. In an alternative preferred embodiment of the method of the invention the mammal is a human and the method comprises testing a biological sample from the human for increased expression of DAPK1 and DAPK2 and decreased expression of NES and EMP1 whereby to predict an increased likelihood of response to gefitinib.

According to another aspect of the invention there is provided an isolated set of marker genes identified as having differential expression between tumour cells that are sensitive and resistant to an erbB receptor drug said gene set comprising one or more genes selected from at least the group consisting of the genes listed in Table 1 defined herein or DAPK2, including gene specific oligonucleotides derived from said genes. Preferably the set comprises at least 2

genes, more preferably at least 3 genes, more preferably at least 4 genes. More preferably the set comprises at least one gene selected from Table 2 as defined herein.

According to another aspect of the invention there is provided an isolated set of marker genes identified as having differential expression between tumour cells that are sensitive and resistant to an erbB receptor drug said gene set comprising one or more genes selected from at least the group consisting of the genes listed in Table 1 defined herein, including gene specific oligonucleotides derived from said genes. Preferably the set comprises at least 2 genes, more preferably at least 3 genes. More preferably the set comprises at least one gene selected from Table 2 as defined herein.

The present invention permits the improved selection of a patient, having or suspected of having a tumour, for treatment with an erbB receptor drug, in order to predict an increased likelihood of response to the erbB receptor drug.

In one embodiment, the method comprises testing a biological sample from the mammal for expression of at least one or more of the following from Table 1, which are found at lower levels in sensitive cells NPAS2, NES, CHST7, ACOX2 or GSPT2 or at least one or more of the following which are found at higher levels in sensitive cells DAPK1 or TNNC1. The Affymetrix ID and Affymetrix probe sequence for these genes are displayed in Table 1. In a preferred embodiment, the method further comprises testing a biological sample from the mammal for expression of DAPK2 which is found at higher levels in sensitive cells, whereby to predict an increased likelihood of response to the erbB receptor drug.

In an alternative embodiment, the method comprises testing a biological sample from the mammal for expression of at least one or more of the following from Table 1, which are found at lower levels in sensitive cells NES, GSPT2, ETR101, TAZ, CHST7, DNAJC3, NPAS2, PIN1, TCEA2 or VAMP4 or at least one or more of the following which are found at higher levels in sensitive cells DAPK1, DAPK2, MLLT3, TNNC1 or KIAA0931. The Affymetrix ID and Affymetrix probe sequence for these genes are displayed in Table 1.

In a preferred embodiment, the method further comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 2, whereby to predict an increased likelihood of response to the erbB receptor drug. In a preferred embodiment, the method comprises testing a biological sample from the mammal for expression of any one of the following genes listed in Table 2, which are found at lower levels in sensitive cells EMP1, SLC20A1, SPRY2 or PGM1, whereby to predict an increased likelihood of response to the

erbB receptor drug. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

In an alternative preferred embodiment, the method further comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 2, whereby to predict an increased likelihood of response to the erbB receptor drug. In a preferred embodiment, the method comprises testing a biological sample from the mammal for expression of any one of the following genes listed in Table 2, which are found at lower levels in sensitive cells EMP1, HCA127, UBL5, ZNF23, UROD, CD44, SPRY1, RAPGEF2, SLC20A1, NRP1, PGM1 or SPRY2 or at least one or more of the following which are found at higher levels in sensitive cells PTGER3, SCN10A, KITLG, CDH1, HOP, BCL3 or OLFM1 whereby to predict an increased likelihood of response to the erbB receptor drug. More preferably the method comprises testing a biological sample from the mammal for expression of EMP1.

In an especially preferred embodiment the method comprises testing a biological sample from the mammal for expression of NPAS2, NES, CHST7, DAPK1 and EMP1. High NPAS2, NES, CHST7 and EMP1 levels are associated with resistance to gefitinib and high DAPK1 levels are associated with sensitivity to gefitinib. Preferably, the assessment of expression comprises determination of whether DAPK1 levels are increased and NPAS2, NES, CHST7 and EMP1 levels are reduced.

In an alternative especially preferred embodiment the method comprises testing a biological sample from the mammal for expression of DAPK1, DAPK2, NES and EMP1. High EMP1 and NES levels are associated with resistance to gefitinib and high DAPK1 and DAPK2 levels are associated with sensitivity to gefitinib. Preferably, the assessment of expression comprises determination of whether DAPK1 and DAPK2 levels are increased and EMP1 and NES levels are reduced. In a most preferred embodiment the invention comprises determining the level of DAPK1 and EMP1.

According to another aspect of the invention there is provided a method for predicting clinical outcome of treatment with an erbB receptor drug for a mammal, having or suspected of having a tumour, comprising determining the level of any of the genes as described hereinabove in a biological sample taken from the tumour, or suspected tumour, wherein a poor outcome is predicted if:

a) the expression level of DAPK1 is reduced; and /or

b) the expression level of NPAS2, NES, CHST7 and EMP1 is increased.

According to another aspect of the invention there is provided a method for classifying cancer comprising, determining the level of any of the genes as described hereinabove in a biological sample taken from a tumour, or suspected tumour, wherein tumours expressing elevated levels of DAPK1 and / or reduced levels of NPAS2, NES, CHST7 or EMP1 are predicted as sensitive to treatment with erbB receptor drugs.

According to another aspect of the invention there is provided a method for predicting clinical outcome of treatment with an erbB receptor drug for a mammal, having or suspected of having a tumour, comprising determining the level of any of the genes as described hereinabove in a biological sample taken from the tumour, or suspected tumour, wherein a poor outcome is predicted if:

a) the expression level of DAPK1 or DAPK2 is reduced; and /or

b) the expression level of EMP1 or NES is increased.

According to another aspect of the invention there is provided a method for classifying cancer comprising, determining the level of any of the genes as described hereinabove in a biological sample taken from a tumour, or suspected tumour, wherein tumours expressing elevated levels of DAPK1 or DAPK2 and / or reduced levels of EMP1 or NES are predicted as sensitive to treatment with erbB receptor drugs.

According to another aspect of the invention there is provided a method for treating a disease condition in a mammal having, or suspected of having, a tumour, predicted to be resistant or non responsive to erbB receptor drug treatment based on the level of any of the genes as described hereinabove, comprising: providing a resistance-surmounting quantity of an erbB receptor drug and administering the resistance-surmounting quantity of the erbB receptor drug to the mammal.

In a preferred embodiment the mammal is a primate. In a most preferred embodiment the mammal is a human. In a preferred embodiment the patient is a primate. In a most preferred embodiment the patient is a human.

The term "erbB receptor drug" includes drugs acting upon the erbB family of receptor tyrosine kinases, which include EGFR, erbB2 (HER), erbB3 and erbB4 as described in the background to the invention above. In a preferred embodiment the erbB receptor drug is an erbB receptor tyrosine kinase inhibitor. In a preferred embodiment the erbB receptor drug is an EGFR tyrosine kinase inhibitor.

In a more preferred embodiment the EGF receptor tyrosine kinase inhibitor is selected from gefitinib, Erlotinib (OSI-774, CP-358774), PKI-166, EKB-569, HKI-272 (WAY-177820), lapatinib (GW2016, GW-572016), canertinib (CI-1033, PD183805), AEE788, XL647, BMS 5599626 or any of the compounds as disclosed in WO03/082831, WO05/012290, WO05/026157, WO05/026150, WO05/026156, WO05/028470, WO05/028469, WO2004/006846, WO03082831, WO03/082290 or PCT/GB2005/000237.

In another preferred embodiment the erbB receptor drug is an anti-EGFR antibody such as for example one of cetuximab (C225), matuzumab (EMD-72000), panitumumab (ABX-EGF/ rHuMAb-EGFr), MR1-1, IMC-11F8 or EGFRL11.

We contemplate that erbB receptor drugs may be used as monotherapy or in combination with other drugs of the same or different classes. In an especially preferred embodiment the EGF receptor tyrosine kinase inhibitor is gefitinib.

In a preferred embodiment the present invention is particularly suitable for use in predicting the response to the erbB receptor drug as described hereinbefore in those patients or patient population with a tumour which is dependent alone, or in part, on an erbB tyrosine kinase receptor. Such tumours include, for example, non-solid tumours such as leukaemia, multiple myeloma or lymphoma, and also solid tumours, for example bile duct, bone, bladder, brain/CNS, glioblastoma, breast, colorectal, cervical, endometrial, gastric, head and neck, hepatic, lung, muscle, neuronal, oesophageal, ovarian, pancreatic, pleural/peritoneal membranes, prostate, renal, skin, testicular, thyroid, uterine and vulval tumours.

In a preferred embodiment the present invention is particularly suitable for identifying a patient with head, neck, pancreatic, glioblastoma, colorectal or breast tumour for drug treatment. In an especially preferred embodiment the present invention also is particularly suitable for identifying those patients with NSCLC, more particularly advanced NSCLC including advanced adenocarcinoma that will respond to treatment with an erbB receptor drug as hereinbefore defined.

The present invention provides advantage in the treatment of tumours such as NSCLC, especially advanced NSCLC by identifying "individual cancer profiles" of NSCLC and so determining which tumours would respond to erbB receptor drug such as gefitinib.

The present invention is particularly useful in the treatment of patients with advanced NSCLC who have failed previous chemotherapy, such as platinum-based chemotherapy. The present invention is also particularly useful in the treatment of patients with locally advanced

(stage IIIB) or metastasized (stage IV) NSCLC who have received previous chemotherapy, such as platinum-based chemotherapy. The present invention is also useful in adjuvant therapy or as a first-line therapy.

In a preferred embodiment there is provided a method of selecting a human, having or suspected of having a tumour, for treatment with gefitinib which comprises testing a biological sample, from the mammal for expression of NPAS2, NES, CHST7, DAPK1 and EMP1, whereby to predict an increased likelihood of response to gefitinib.

In a preferred embodiment there is provided a method of selecting a human, having or suspected of having a tumour, for treatment with gefitinib which comprises testing a biological sample, from the mammal for expression of DAPK1, DAPK2, NES and EMP1 whereby to predict an increased likelihood of response to gefitinib.

According to another aspect of the invention there is provided a method of predicting the responsiveness of a patient or patient population with cancer, for example lung cancer, to treatment with chemotherapeutic agents, especially erbB receptor drugs, comprising comparing the differential expression of any of the genes described herein.

In one embodiment the assessment of expression is performed by gene expression profiling using oligonucleotide-based arrays or cDNA-based arrays of any type, particularly where large numbers of genes are analysed simultaneously. In an alternative embodiment, RT-PCR (reverse transcription- Polymerase Chain Reaction), real-time PCR, *in-situ* hybridisation, Northern blotting, Serial analysis of gene expression (SAGE) for example as described by Velculescu et al Science 270 (5235): 484-487, or differential display or any other method of measuring gene expression at the RNA level could be used. Details of these and other general molecular biology techniques can be found in Current Protocols in Molecular Biology Volumes1-3, edited by F M Asubel, R Brent and R E Kingston; published by John Wiley, 1998 and Sambrook, J. and Russell, D.W., Molecular Cloning: A Laboratory Manual, the third edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001.

In another embodiment the assessment of expression is performed by measurement of protein levels encoded by the aforementioned genes. For example, an immunohistochemistry-based assay or application of an alternative proteomics methodology.

In another embodiment the assessment of expression is performed by measurement of activity of the proteins encoded by the aforementioned genes, for example in a bioassay.

In a preferred embodiment the biological sample would have been obtained using a

minimally invasive technique to obtain a small sample of tumour, or suspected tumour, from which to determine gene expression profile. Such techniques include, for example tumour biopsy, such as transbronchial biopsy. The profile of gene expression of transbronchial biopsy specimens whose size is about 1 mm may be measured for example using a suitable amplification procedure.

Another aspect of the invention provides a kit for use in a method of predicting the responsiveness of a patient or patient population with a tumour, to treatment with chemotherapeutic agents, especially erbB receptor drugs, comprising a means for measuring the levels of any of the genes as described hereinabove. Preferably the genes are attached to a support material or membrane such as nitrocellulose, or nylon or a plastic film or slide.

In a further preferred embodiment the present invention includes administration of an erbB receptor drug to a mammal selected according the methods described hereinabove.

According to another aspect of the invention there is provided a method of using the results of the methods described above in determining an appropriate dosage of an erbB receptor drug.

In a preferred embodiment the biological sample comprises either a single sample which may be tested for expression of any of the genes as described hereinabove, or multiple samples which may be tested for expression of one or more of the genes as described hereinabove.
The invention is illustrated by the following non-limiting examples in which:
Fig 1 illustrates a xenograft (A549 cell line) which when grown as a xenograft in athymic mice is sensitive to gefitinib. This involved oral dosing, once daily, at the dose indicated. Y axis = mean tumour volume in cm^3; x axis = days after treatment.
Fig 2 illustrates a xenograft (MKN45 cell line) which when grown as a xenograft in athymic mice is resistant to gefitinib. This involved oral dosing, once daily, at the dose indicated. Y axis = mean tumour volume in cm^3; x axis = days after treatment.
Figures 3, 4, 5 and 6 show examples of specific gene expression profiled across a wider panel of gefitinib sensitive and resistant lines, where definition of sensitivity is based on response to gefitinib when grown as a xenograft, to increase confidence that the expression profile of each gene is truly predictive. Iressa sensitivity is based on xenografts data. The cell lines and the tumours from which they are derived are as follows; KB – head and neck, HT29 - colon, BT474 – breast, DU145 – prostate, LoVo – colon, MCF7 – breast, GEO – colon, A549 – lung,

A431 - epidermoid, H322 – lung, HX147 – lung, RT112 – bladder, MiaPaCa2 – pancreas, MKN45 – gastric, MDAMB231 – breast, PC3 - prostate, Calu6 – lung, SW620 – colon. The legend key is S=sensitive, U=unknown and R=resistant.

Fig 3 shows EMP1 basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Fig 4 shows DAPK1 basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Fig 5 shows DAPK2 basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Fig 6 shows NES basal expression in Cell Culture - wider cell panel (Taqman RT-PCR).

Example 1

Gene Expression in Gefitinib Resistant or Sensitive Tumour Cell Lines – Cell Culture and Xenograft Studies

We identified genes useful to predict response to erbB receptor drugs in the clinic. This is based on studies with gefitinib, but the findings are applicable to erbB receptor drugs in general.

The gene lists have been assembled by comparing tumour cell lines which have been demonstrated to be either sensitive to gefitinib or resistant to gefitinib. This definition is based on the response observed when the tumour cell line is implanted into nude mice and grown as a xenograft. This definition has been used for all the pre-clinical studies described herein.

Initially a small panel of six human tumour cell lines were assembled, three which are sensitive to gefitinib and three which are resistant to gefitinib in the xenograft setting defined above.

The sensitive cell lines were;

1. Lovo (ATCC[1] No. CCL-229) – colon tumour cell line
2. KB (ATCC No. CCL-17) – initially reported as a nasopharyngeal cell line (although more recently reported as Hela derived (cervical carcinoma)
3. HT29 (ATCC No. HTB-38) – colon tumour cell line

The resistant cell lines were;

1. MKN 45 (source - Nottingham University, UK) – gastric tumour cell line
2. Calu 6 (ATCC No. HTB-56) – lung tumour cell line
3. PC3 (ATCC No. CRL-1435) – prostate tumour cell line

[1]ATCC = American Type Culture Collection

The cell lines were grown both in cell culture and as xenografts, RNA prepared and the basal expression profiles determined by measuring RNA expression on the Affymetrix microarray platform. As part of our studies, the term 'basal' has been used to indicate constitutive or steady state expression levels (rather than expression levels which are modulated as a consequence of administration of an erbB ligand or gefitinib to the cells). Figure 1 illustrates the sensitivity of A549 xenografts (used in Example 3 below) to treatment with gefitinib. Figure 2 illustrates the resistance of MKN45 xenografts to gefitinib. See Example 2 below for analysis of results.

Example 2

Statistical analyses of cell culture and xenograft data sets

The following statistical analyses were performed separately for cell culture and xenograft data sets. Probe sets were eliminated if their signal was not distinguishable from background noise across all RNA samples in the set. Mixed ANOVA (see for example Scheffe, 1959) was applied separately to each remaining probe set to generate p values. The p values were then used to calculate Q values (Storey). The Q values indicate the expected proportion of genes in a gene list which are not truly differentially expressed but have been falsely discovered (False Discovery Rate or FDR). Q value cut-offs appropriate in the different studies were identified and applied, based on graphical examination of the p value and Q value results, in conjunction with fold change. The final genelists for each study were generated using Q value and fold change (FC) cut-offs. The different genelists were then combined to display an overall list of genes which showed consistent differences in expression profiles between the cell lines in the sensitive and resistant groups.

Further details of the analysis procedures are provided as follows. Fold change (FC) was calculated based on the mean of sensitive cells divided by the mean of resistant cells. To generate gene lists, FC cut-off of two-fold (2X) change in either direction was used in all cases. Furthermore FDR Q values were used to narrow down the lists and obtain the most significant gene changes across sensitive versus resistant cell lines. In the case of cell culture, Q value cut-off is 0.3. In the case of xenograft, Q value cut-off is 0.6. The different cut-offs used reflect the different design and variance values associated with each experiment.

In cell culture studies, lists were obtained based on the above criteria for cells grown either in full serum containing medium or in charcoal stripped serum. In the xenograft study, the same as above was performed for separate sets of tumours harvested at 18hr intervals. Gene lists contain some redundancy in genes where appropriate to illustrate consistency of results obtained for example with different probe sets.

Example 3

Identification of predictive genes

Genes which have not previously been identified as predictive of erbB receptor drug sensitivity are listed in Table 1. Other genes which we have identified to be optionally used in combination with Table 1 genes are listed in Table 2.

Key to Tables:

'Affymetrix ID' – the Affymetrix probe set identifier

'Sequence' – target sequence relating to the Affymetrix probe set indicated by 'Affymetrix ID'

"+ if up in sensitive" means that the gene is relatively highly expressed in sensitive cells. (Consequently, absence of a "+" means that the gene is relatively highly expressed in resistant cells).

'Gene Title'- The current annotation of the gene relating to 'Affymetrix ID' based on UniGene 133

'Gene Symbol' – shorthand synonym for the gene title

'Locus Link' & RefSeq Transcript ID' are provided for gene identification purposes.

Combining genes has the potential to generate an improved diagnostic over genes used in isolation. Collective gene expression profiles (at the RNA and/ or protein level) may be more likely to identify patients most likely to benefit from gefitinib rather than the expression level of one gene in isolation.

It may be more practical when developing a pre-treatment response prediction diagnostic to work with a truncated gene list from tables 1 and / or 2. A number of criteria have been used to shorten the gene list to identify those genes which are most predictive of response. Firstly the statistical (p values and Q values or FDR values) can indicate the statistical significance of a gene.

Secondly, the differential expression (fold change) between the sensitive and resistant groups indicates the potential sensitivity of a marker to be used in a diagnostic test (highest fold change between sensitive group and resistant group is preferred).

Thirdly, we have performed RT-PCR based expression profiling across a wider panel of gefitinib sensitive and resistant human tumour cell lines to increase confidence that the expression profile of each gene is truly predictive. Figs 3, 4, 5 and 6 show examples of specific gene expression profiled across a wider panel of cell lines as set out below.

The sensitive human tumour cell lines, where definition of sensitivity is based on response to Iressa when grown as a xenograft:

a. BT474 (ATCC No. HTB-20) – breast tumour cell line
b. DU145 (ATCC No. HTB-81) – colon tumour cell line

c. MCF7 (ATCC No. HTB-22, sourced from ICRF (now CR-UK), London), - breast tumour cell line
d. GEO colon tumour cell line. RNA obtained from Fortunato Ciardiello, Cattedra di Oncologia Medica, Dipartimento Medico-Chirurgico di Internistica Clinica e Sperimentale "F. Magrassi e A. Lanzara, " Seconda Universita delgi Studi di Napoli, Via S. Pansini, 5-80131, Naples, Italy.
e. A549 (ATCC No. CCL-185) – lung tumour cell line
f. A431 (ATCC No. CRL-155) – epidermoid cell line

The resistant human tumour cell lines, where definition of sensitivity is based on response to Iressa when grown as a xenograft:

1) HX147 - (source: ICRF (now CR-UK), London) – lung tumour cell line
2) RT112 - bladder tumour cell line (DSMZ No ACC 418)
3) MiaPac2 (ECACC 85062806, ref. no. 001611) pancreatic tumour cell line
4) MDAMB231 (ATCC No. HTB-26) – breast tumour cell line
5) SW620 (ECACC CCL-227) – colon tumour cell line

ATCC = American Type Culture Collection

DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (German Collection of Micro-organisms and Cell Cultures)

ECACC = European Collection of Cell Cultures

In isolation, each of these genes is reasonably predictive of gefitinib response, but collectively they can be applied to make predictions with a higher level of confidence.

The Affymetrix probe sets identifiers for the genes in the above diagnostic genelists are indicated in Tables 1 and 2. Current Affy IDs are based on Affy U133 chipset. For the avoidance of doubt, the target sequences of the Affymetrix probe sets which identified the listed genes are also provided in Tables 1 and 2.

Without wishing to be bound by theoretical considerations, it is contemplated that the specific sequences used to detect target genes in the Examples may define specific splice variants or sequences in homologous genes. Therefore in one embodiment, a listed gene for use in the method of the invention is defined by the specific sequence used in said Examples. In another embodiment, a gene for use in the method of the invention is not limited by the specific sequence used in these Examples. Indeed the fact that some genes in Tables 1 and 2 have been identified using different sequences (gene "redundancy") and confirmatory RT-PCR studies (see

Example 4) provides evidence that usefulness in the method of the invention is not generally limited to the specific sequences used to measure the target gene.

Note, in the event of a discrepancy in the sequence between Tables 1 and 2 and the Sequence Listing, the sequence as provided in the Tables is preferred.

Table 1: **as described in priority application US60/619027 filed on 18/10/2004.**

Gene Symbol	Gene Title	Affymetrix ID	+ up in sensitive	Sequence	LocusLink	RefSeq Transcript ID	SEQ ID NO.
ACOX2	"acyl-Coenzyme A oxidase 2, branched chain / acyl-Coenzyme A oxidase 2, branched chain"	205364_at		Gtgcagcatttacagaccctgacgcaatccggagctgaccagcacgaggcttgga accagaccactgtcatacacctccaggctgctaaggtgcactgctactatgtcactgtg aagggttttacagaagctctggagaaactagaaaatgaaccagcgattcagcaggt gctcaagcgcctctgtgacctccatgccatacatggaatcttgactaactcgggtgact ttctccatgacgccttcctgtctggtgcccaagtggacatggcaagaacagcctacctg gacctgctccgcctgatccggaaggatgccatcctgttaactgatgcttttgacttcacc gatcagtgtttaaattcagcccttggctgttatgatggaaacgtctacgaacgcctgttcc agtgggctcagaagtc	8309	NM_003500	SEQ ID NO:1
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	200729_s _at		gagcttaagatctggtgttttgttaatgcttctgtttattccagaagcattaaggtaacccat tgccaagtatcattcttgcaaattattcttttatataactgaccagtgcttaataaaacaag caggtacttacaaataattactggcagtaggttataattggtggtttaaaaataacattg gaatacaggacttgttgccaattgggtaattttcattagttgttttgtttgttttgatttgaaac ctggaaatacagtaaaatttgactgtttaaaatgttggccaaaaaaatcaagatttaatt tttttatttgtactgaaaaactaatcataactgttaattctcagccatctttgaagcttgaaa gaagagtctttggtattttgtaaacgttagcagactttcctgccagtgtcagaaaatccta tttatgaatcctgtcggtattccttggtatctgaaaaaaataccaaatagtaccatacatg agttatttctaa	10097	NM_005722	SEQ ID NO:2
APOL1	"apolipoprotein L, 1 / apolipoprotein L, 1"	209546_s _at	+	agaatagagaggaggcttgaaggaaccagcaatgagaaggccaggaaaagaa agagctgaaaatggagaaagcccaagagttagaacagttggatacaggagaaga aacagcggctccactacagacccagccccaggttcaatgtcctccgaagaatgaag tctttccctggtgatggtcccctgccctgtctttccagcatccactctcccttgtcctcctgg gggcatatctcagtcaggcagcggcttcctgatgatggtcgttggggtggttgtcatgtg atgggtccctccaggttactaaagggtgcatgtcccctgcttgaacactgaagggcag gtggt	8542	NM_003661 / NM_145343 / NM_145344	SEQ ID NO:3
C10orf 10	chromosome 10 open reading frame 10 / chromosome 10 open reading frame 10	209183_s _at		aactcatacgtcctgtggtggcattgggagagttcccccatgatgagggccaagata gaatctgtaccactcagtgctaccatccccacccctacaccacttccacacaggggc ctcatggcatggtcagggtcccagctgtaggtgagagcagggcactgtccagctgtc cactggggaagtcaagatgtcctaaggcccaggtcagggcatctggagtctgaagg accctagttcctagaggcatctggcagcaagaaggtgaggcatcagggaacggga atcaggctgggactgatcagaggtgaagggacagagagaggagaggaggaaga ttgagctgggggcaacagccaagctcacctgggcaggtctctgccacctccttgctct gtgagctgtcagtctaggttattctctttttttgtggctatttttaattgctttggatttgttaaatg ttttctgtcttctgttaagtgtgttt	11067	NM_007021	SEQ ID NO:4

CALM1	"calmodulin 1 (phosphorylase kinase, delta)"	211984_at		tgaacggctgtgcagtaggcccagcgctgctgtgtctcgtcagaggaatagcttacca cgaacccctcagcatactgggaatctcttcctgaacaacgaatgtaaatttggtcaagt ctactcttccgttcattcaattatttaagcatttgaattatttattgtatatcctaaatatatttct cctttggcagtgactagatttccactaatgtgtcttaatctatccctccagctggcagttac tgtttttttaatcccctgaagttgtcctgtaggagacagaaattctttgctgtctgtatccctt ggagtaa	801	NM_006888	SEQ ID NO:5
CALM1	"calmodulin 1 (phosphorylase kinase, delta)"	211985_s_at		gaggcaaatggatctcgatatttcagatgggcttttgatgcactgttgccaaggaaggc tttttctgattttttgacaaatgaatttttgcacactttcattggtgtctttcggcaacttacaca cattgaaaat	801	NM_006888	SEQ ID NO:6
CD44	CD44 antigen (homing function and Indian blood group system)	210916_s_at		caagttttggtggcacgcagcctggggactctgcctcgtgccgctgagcctggcgca gatcgatttgaatataacctgccgctttgcaggtgtattccacgtggagaaaaatggtc gctacagcatctctcggacggaggccgctgacctctgcaaggctttcaatagcacctt gcccacaatggcccagatggagaaagctctgagcatcggatttgagacctgcagttt gcattgcagtcaacagtcgaagaaggtgtgggcagaagaaaaagctagtgatcaa cagtggcaatggagctgtggaggacagaaagccaagtggactcaacggagaggc cagcaagtctcaggaaatggtgcatttggtgaacaaggagtcgtcagaaactccag accagt	960	NM_000610	SEQ ID NO:7
CD44	CD44 antigen (homing function and Indian blood group system)	212063_at		attgtaaatcttttgtgtctcctgaagacttcccttaaaattagctctgagtgaaaaatcaa aagagacaaaagacatcttcgaatccatatttcaagcctggtagaattggcttttctag cagaacctttccaaaagttttatattgagattcataacaacaccaagaattgattttgtag ccaacattcattcaatactgttatatcagaggagtaggagagaggaaacatttgactta tctggaaaagcaaaatgtacttaagaataagaataacatggtccattcacctttatgtta tagatatgtctttgtgtaaatcatttgttttgagttttcaaagaatagcccattgttcattcttgt gctgtacaatgaccactgttattgttactttgacttttcagagcacaccc	960	NM_000610	SEQ ID NO:8
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	212864_at		ttctatgcatccacaccaaaatcctgcagaatgtaagtaagctctgctttataagatgg gttcaccttcatcgcagactgaaagtttcagtttttattttttncagaaagcacgaaaaat tatttataatagtctggagaaaaaacacactgtaatatttcaagtgtatgcagtagaatg tactgtaactgagccctttcccacatgtctaggctccaatgtctcctgtaggtccacctaa ctgtgtgttttcagggacaatgccatccatgtttgtgctgtagacttgctgctgctgaatcct ttctggggactttctcatcgggcagggagcagagggcttctcgttcatgcaccctttgcc tgaacacccatgtagctgctgtgttgtgtatatattactcttaagaggagtgtgtgtgtctgt gtttgttttaaaagtcacttatttcttacagtgatttcaattgcaccatgacttcttcactaaa accacaaagtcctgcttaaaactatggaaaacctaacctgattagagccttgac	8760	NM_003818	SEQ ID NO:9

CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7 / carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	206756_at		ggcaatctgtcacactctcagagtctgggacttgacttgctaccaacaactgctgtgcaattctgctgagcaggaatatcatgagctgttcaataatgacggacgcattggttgagatgaagtttccagtaaggaagtgacagtgcaatgtggatatttatggctgtaaaataggaagagctttagttcccaggctgaacctgccactgctggagccatttcaacaaggcatcctcacaacaaagaagagatgtgatttggtaccatttcacaccagcaggtgtctggacgaaaacatcaatgtgaataagggccaagtgcagtcctgtcttgattaaattacttaataatattattaaataataataggtctgggcagtattgtttttaacctgactcatccagctgtccttcaaatagctccgtctccctctacccagaactgatttttaaaaagaagtaatttttctccctgggctgggaaaaccctaatgaactgaaacacacttttactttaaaatttttctgtctggcgttttgtaatc	56548	NM_019886	SEQ ID NO:10
COMMD3	COMM domain containing 3	218048_at		gaattccctagaaatcctactgggaagtataggcagatctctccctcatataacggatgtttcttggcgcttggaatatcagataaagaccaatcaacttcataggatgtacagacctgcatatttggtgaccttaagtgtacagaacactgattccccatcctatccagagattagttttagttgcagcatggaacaattacaggacttggtggggaaacttaaagatgcttcgaaaagcctggaaagagcaactcagttgtaacttggggaagttaacgatccgcccgagtgcagaggaaaaccagaaacgccttgccttcagctgaaccaccgtttgtgcgagctggatgtccttttcagtagaaaagaattttcctttgaatttataccattcatcaattttgacactttaaaaacgtgtgaaagggttaagagggaaagatactgcccaagtatttgaatcgtttagtagtaactgtccatttatcctat	23412	NM_012071	SEQ ID NO:11
CUL2	cullin 2 / cullin 2	203078_at		tataatacttcagtaaggcctttaaaaaatccacagtgatattattactcctaacaaaaacaataattacttagtatcatctaatatgtggttcatatttaaatttgttgttttgagatgggtcttacaattggtttattcaattgcatttttctaactcgtgtctcaagtgttttaaaaatctactgnacttataatgacttatataatgtatttctcattttacctttcttccaaaagaggaaataatggcaaaccatataatattgtacattcactgtcaaaaagcaaacccttgttttgataacttgt	8453	NM_003591	SEQ ID NO:12
DAPK1	death-associated protein kinase 1 / death-associated protein kinase 1	203139_at	+	cctcctccagggtgattttatgatcagtgttgttgctctaggaagacatttttccgtttgcttttgttccaatgtcaatgtgaacgtccacatgaaacctacacactgtcatgcttcatcattccctctcatctcaggtagaaggttgacacagttgtagggttacagagacctatgtaagaattcagaagacccctgactcatcatttgtggcagtcccttataattggtgcatagcagatggtttccacatttagatcctggtttcataacttcctgtacttgaagtctaaaagcagaaaataaaggaagcaagttttcttccatgattttaaattgtgatcgagttttaaattgataggagggaacatgtcctaattcttctgtcctgagaa	1612	NM_004938	SEQ ID NO:13
DNAJC3	"DnaJ (Hsp40) homolog, subfamily C, member 3"	208499_s_at		aggagaggatttgccactgcttttctaaggacgagaagcctgttgaagctattagggtttgttctgaagttttacagatggaacctgacaatgtgaatgccctgaaagatcgagctgaggcctatttgatagaggaaatgtatgatgaagctattcaggattatgaaactgctcaggaacacaatgaaaatgatcagcagattcgagaaggtctagagaaagcacaaagattattgaaacagtcgcagaaacgagattattataaaatcttgggagtaaaaagaaatgccaaaaagcaagaaattattaaagcataccgaaaattagcactgcagtggcacccagataacttccagaatgaagaagaaaagaaaaaagctgagaaaaagttcattgatatagcagctgctaaagaagtcctctctgatccagaaatgagaaagaagtttgacgacggagaagatcctttggatgcagagagccagcaaggaggcggcggcaaccctttccacagaagctggaactcatggcaagggttcaatcccttcagctcaggcggaccatttaga	5611	NM_006260	SEQ ID NO:14

DPYSL 3	dihydropyrimidinase-like 3 / dihydropyrimidinase-like 3	201431_s_at		tgagggccacgggcttgggtagtggaaagggtgtttgggaaattgttaaatcagttacccgtagtagagctatttcttgtacttctaagttttctagaagtggaaggattgtagtcatcctgaaaatgggtttacttcaaaatccctcagccttgttcttcacgactgtctatactgagagtgtcatgtttccacaaagggctgacacctgagcctggattttcactcatccctgagaagccctttccagtagggtgggcaattcccaacttccttgccacaagcttcccaggctttctcccctggaaaactccagcttgagtcccagatacactcatgggctgccctgggcagccagcattcattgtaagttccctctttgaaaactggtgtgtgggtgttcagttctgtgtctggtgggtatggacagacagtaatctcctgtgatctgtgctagctgtgaggcagctctggaacgtga	1809	NM_001387	SEQ ID NO:15
DUSP4	dual specificity phosphatase 4 / dual specificity phosphatase 4	204015_s_at		ggctcccagcaagggtaggacgggccgcatgcgggcagaaagttgggactgagcagctgggagcaggcgaccgagctccttccccatcatttctccttggccaacgacgaggccagccagaatggcaataaggactccgaatacataataaaagcaaacagaacactccaacttagagcaataacggctgccgcagcagccagggaagaccttggtttggtttatgtgtcagtttcacttttccgatagaaatttcttacctcatttttttaagcagtaaggcttgaagtgatgaaacccacagatcctagcaaatgtgcccaaccagctttactaaagggggaggaagggagggcaaagggatgagaagacaagtttcccagaagtgcctggttctg	1846	NM_001394 / NM_057158	SEQ ID NO:16
EIF3S4	"eukaryotic translation initiation factor 3, subunit 4 delta, 44kDa / eukaryotic translation initiation factor 3, subunit 4 delta, 44kDa"	208887_at		gatacgctggggcccatgcagaaggagctggccgagcagctgggcctgtctactggcgagaaggagaagctgccgggagagctagagccggtgcaggccacgcagaacaagacagggaagtatgtgccgccgagcctgcgcgacggggccagccgccgcggggagtccatgcagcccaaccgcagagccgacgacaacgccaccatccgtgtcaccaacttgtcagaggacacgcgtgagaccgacctgcaggagctcttccggcctttcggctccatctcccgcatctacctggctaaggacaagaccactggccaatccaagggctttgccttcatcagcttccaccgccgcgaggatgctgcgcgtgccattgccggggtgtccggctttggctacgaccacctcatcctcaacgtcgagtgggccaagccgtccaccaactaagccagctgccactgtgtactcggtccgggacccttggcgacagaagacagcc	8666	NM_003755	SEQ ID NO:17
EIF5A	eukaryotic translation initiation factor 5A	213757_at		atgtgtcggggagagagcccgcagggaagggtaaagcccannggggcagggccctcccagatgcctgaggagggggcaggtcccctcccctctcctcctcttccctccccatctaaaggggtttggggagagacacaggcaggcgagggggctggtccccagtctgttggggtggtgctcagggtaaagggctatnggcaacaggggaccagaccagggatgagtggggagggcacaaggaccatttgccagaatccaccg	1984	NM_001970	SEQ ID NO:18
FADS2	fatty acid desaturase 2 / fatty acid desaturase 2	202218_s_at		ctgttgctccaggatgcattctgataggagggggcggcagggctgggccttgtgacaatctgcctttcaccacatggccttgcctcggtggccctgactgtcagggagggccagggaggcagagcgggagggagtctcaggaggaggcttgccctgaggggctggggaggggggtacctcatgaggaccagggtggagcttgagaagaggaggaggtgggggcttggaggtgcttggtagctgaggggacgggcaagtgagaggggagggagggaagtcctgggaggatcctgagctgctgttgcagtctaacccactaatcagttcttagattcagggggaagggcaggcaccaacaactcagaatgggggctttcggggagggcgcctagtccccccagctctaagcagccaggagggacctgcatctaagcatctgggttgccatggcaatggcatgcccccccagctactgtatgcccccgacccccgcagaggcagaatgaacccatagggagctgatcgtaat	9415	NM_004265	SEQ ID NO:19

FLJ12442	hypothetical protein FLJ12442	218051_s_at		gggaccacctctatagtgatctggcggatctcatgctgcggcacggctggcgcacaggcgccatcatccccgagctggagcgtgagatccgcatcatcaacacggagcagtacatgcactcgctgacgtggcagcaggcgctcacggggctgctggagcgcatgcagacctatcaggacgcggagtcgaggcaggtgctggctgcctggatgaaagagcggcaggagctgaggtgcatcaccaaggccctgttcaatgcgcagttcggcagcatcttccgcaccttccacaaccccacctacttctcaaggcgcctcgtgcgcttctctgacctctacatggcctccctcagctgcctgctcaactaccgcgtggacttcaccttctacccacgccgtacgccgctgcagcacgaggcacccctctggatggaccagctctgcaccggctgcatgaagacccccttccttggtgacatggcccacatccgctgagggcacctttattgtctgggac	64943	NM_022908	SEQ ID NO:20
FLJ22028	hypothetical protein FLJ22028	213878_at	+	tattcaaacggagtcctcccattccaagaaactggaaacccctagtttatgttaaaaggccagtctaaattctttcacttacatctttacagaaaactatattttctctcttccatacccagaaatctaatcagaaaactgacttttctcatgttcaactggacctaggggaatatgacagaaaagcatcccataggctttaatatactttttaaaatatataaaactgaaaattaatagccatttaccctgaaagagttctgcgtggactttgtcacttgcatagtaatagcatgtgcctcattgttcagaagattagctttaggtcctattttcaaatacgaaatggtagcataagctgtaaaactgtagtcttctctgcagaaaataaaggccaacaataagaaagcttttgaaggaatcacggaaaacaaatttataaaagaaataactatatgcgcagtaattcttaacacattgac	79912	NM_024854	SEQ ID NO:21
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H2AFY 2	"H2A histone family, member Y2 / H2A histone family, member Y2"	218445_at		cagggatcggaggacgacccgagtcccaagagtggggttttgctttttaaaaggagagaggaggggtgatggcaggggagtggagggtggccgggcaggtcctgccggcgcagggagccctctgcccttcacactctcctccaaaagagcctccatctgtaaggaagcaggtctccgcgaggggtttctttccatgtgttttcctcctgttgttaaaagaactttttaaaaaaacagacctcgttttagatttatagcattgacttttacacacattcacacaagaaaaaaatcctttcaaaattcttaaatcttctgttcctcctttttccaagggaagagggcaaaagtggcctgggctctgttggtgtgcgtgttccgtggcggagagaagaaaatgggaaagacatctcactggtgcttttctcttttgttttagtgcccccgcccccatccctataatatctgtaac	55506	NM_018649	SEQ ID NO:25
HMGA 2	high mobility group AT-hook 2 / high mobility group AT-hook 2 / high mobility group AT-hook 2	208025_s_at		gaagcaattgctcatgttggccaaacatggtgcaccgagtgatttccatctctggtaaagttacacttttatttcctgtatgttgtacaatcaaaacacactactacctcttaagtcccagtatacctcatttttcatactgaaaaaaaaagcttgtggccaatggaacagtaagaacatcataaaatttttatatatatagtttatttttgtgggagataaattttataggactgttctttgctgttgttggtcgcagctaaataagactggacatttaactttctaccatttctgcaagttaggtatgtttgccaggagaaaagtatcaagacgtttaactgcagttgactttctccctgttcctttgagtgtcttctaactttattctttgttctttatgtagaattgctgtctatgattgtactttgaatcgcttgacttgttgaaaatatttctctagtgtattatcactgtctgttctgcacaataaacataacagcctctgtgatccc	8091	NM_003483	SEQ ID NO:26
IER2	immediate early response 2 / immediate early response 2	202081_at		gcgtttccaacctcggagaattccaggcactccccttcccccctccgctgacatacttgtataagcggtcatcgttgcgtcatggggcaggcgtggggagcttcctgtcgccttggctgggtgtgggcctggaggaaggtcctggggcgtgcactcgcctgggcagtggggaggagagtggcctgagttacttcaccccccgcgtgctgctggttaatgtcccgcgtctctgcaccttcgggtgggagcggggactgatctactttcacattctcaagtttttctcatctgcattagaggtccccagtaggttcccaggttccagcgtgcccctccctcagacacacggacacaatcagccgagaagttcctggtctgaatcacgagaatgtggaggggtggggggtgtcagtggaaaggcataaggctgagctgagaccagttgctggtgaaactgggccaatctggggaggggaacatccttgccagggagtttctgagggtctgctttgtttacctttcgtgcggtggattctttttaactccgtctacctggcgttttgttaga	9592	NM_004907	SEQ ID NO:27
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MLLT3	"myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 / myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3"	204918_s_at	+	aaggcattccacaggatcatcatttaaaaaaaaagaattctggtcctgttttctaaaaaaaaaaaactgttgtagaaattcttaatttggatctatttattagtcagagtttcagctttcttcagctgccagtgtgttactcatctttatcctaaaaatctggaatcagagatttttgtttgttcacatatgattctcttagacacttttatatttgaaaaaattaaaatctttctttggggaaaaattcttggttattctgccataacagattatgtattaacttgtagattcagtggttcaatacctgtttagttgcttgctaatatttccagaaggatttcttgtattggtgaaagacggttggggatggggggatttttttgttcttgttgtaccccttgttttgaaactagaaatctgtcctgtggcatgcaaaagaaagcaaattatttttaaaagaaaaaaaccaaagtactttggtgtcattattccatcttctcca	4300	NM_004529	SEQ ID NO:32
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MT1E	metallothionein 1E (functional)	212859_x_at	+	caccgcgcagagctcagggggtggtgcgcccggcccttctgcggcgcacagcccagcccaggaacgcgggcggtgcggactcagcgggccgggtgcaggcgcggagctgggcctctgcgcccggcccganctccgtctataaanagagcagccagttgcagggctcnantctgctttccaactgcctgactgcttgttcgtctcactggtgtgagctccagcatcccctttgctcgaaatggaccccaactgctcttgcgccactggntggctcctgcacgtgcgccggctcctgcaagtgcaaagagtgcaaatgcacctcctgcaagaagagctgctgttcctgctnccccgtggnctgtgccaagtgtgcccagggctgcgtctgcaaaggggcatcggagaagtgcagctgctgtgcctgatgtgggaacagctcttctcccagatgtaaatagaacaacctgcacaacctggnatttttttaaaaatacaacactgagccatttgctgcatttc	4493	NM_175617	SEQ ID NO:34
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PIN1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 / protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	202927_at		agccatttgaagacgcctcgtttgcgctgcggacgggggagatgagcgggcccgtgttcacggattccggcatccacatcatcctccgcactgagtgagggtggggagcccaggcctggcctcggggcagggcagggcggctaggccggccagctccccccttgcccgccagccagtggccgaacccccccactccctgccaccgtcacacagtatttattgttcccacaatggctgggagggggcccttccagattgggggccctggggtccccactccctgtccatccccagttggggctgcgaccgccagattctcccttaaggaattgacttcagcaggggtgggaggctcccagacccagggcagtgtggtgggaggggtgttccaaagagaaggcctggtcagcagagccgccccgtgtcccccaggtgctggaggcagactcgagggccgaattgtttctagttaggccacgctcctctgttcagtcgcaaaggtgaacactcatgcggcagcc	5300	NM_006221	SEQ ID NO:43
PRKCA	"protein kinase C, alpha"	213093_at		gattaaacgactgtgtctttgtcacctctgcttaactttaggagtatccattcctgtgattgtagacntttgttgatattcttcctggaagaatatcattcttttcttgaagggttggtttactagaatattcaaaatcaatcatgaaggcagttactattttgagtctaaaggttttctaaaaattaacctcacatcccttctgttagggtctttcagaatatcttttataaacagaagcatttgaagtcattgcttttgctacatgatttgtgtgtgtgaaggacataccacgtttaaatcattaattgaaaaacatcatataagccccaactttgtttggaggaagagacggaggttgaggttttccttctgtataagcacctactgacaaaatgtagaggccattcaaccgtcaaacaccatttggttatatcgcagaggagacggatgtgtaaattactgcattgctttttttttcagtttgtataacctctaatctccgtttgcatgatacgctttgttagaa	5578	NM_002737	SEQ ID NO:44
RIOK3	RIO kinase 3 (yeast)	202129_s_at		tgaatgtacgcttgtccatgctgacctcagtgagtataacatgctgtggcatgctggaaaggtctggttgatcgatgtcagtcagtcagtagaacctacccaccctcacggcctggagttcttgttccgggactgcaggaatgtctcgcagtttttccagaaaggaggagtcaaggaagcccttagtgaacgagaactcttcaatgctgtttcaggcttaaacatcacagcagataatgaagctgatttttttagctgagatagaagctttggagaaaatgaatgaagatcacgttcagaagaatggaaggaaagctgcttcattttgaaagatgatggagacccaccactactatatgatgaatagcactaatacccactgcttcagtgttaacacagcagtgattgtcagctgccaatagcaaatgaagttatgggtgacttgaaataccaaaacctgaggagtgggcaatggtgcttctgtg	8780	NM_003831 / NM_145906	SEQ ID NO:45

SERPINB9	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9 / serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9"	209723_at	+	ttcgccacattggccgtgttggtcttgaactcctggcctcaagcaatccgcctacctcag cctcccaaagtgctaggattacaggcataagccactgagcccagccctagttcagta tcttttatgtaaattataaacatctgcaacattatgtatcatatgcagatacttattgcatttct tttattagtggtgaaagtgttctatgcatttattggctcttgaatttcctcatctatgaattgtca ttcacacacctacttttctgcttcgttttacatatgtctttgcctattaaagatattatccctct gttttatatttctctcattcttgtattgcctttaa	5272	NM_004155	SEQ ID NO:46
SIX1	sine oculis homeobox homolog 1 (Drosophila) / sine oculis homeobox homolog 1 (Drosophila)	205817_at		ccggaggcaaagagaccgggccgcggaggccaaggaaagggagaacaccga aaacaataactcctcctccaacaagcagaaccaactctctcctctggaagggggca agccgctcatgtccagctcagaagaggaattctcacctccccaaagtccagaccag aactcggtccttctgctgcagggcaatatgggccacgccaggagctcaaactattctc tcccgggcttaacagcctcgcagcccagtcacggcctgcagacccaccagcatcag ctccaagactctctgctcggccccctcacctccagtctggtggacttggggtcctaagt ggggagggactggggcctcgaagggattcctggagcagcaaccactgcagcgact agggacacttgtaaatagaaatcaggaacattttgcagcttgtttctggagttgtttgcg cataaaggaatggtggactttcacaaatatctttttaaaaatcaaaaccaacagcgat ctcaagcttaa	6495	NM_005982	SEQ ID NO:47
SLCO3A1	"solute carrier organic anion transporter family, member 3A1 / solute carrier organic anion transporter family, member 3A1"	219229_at		ggctgagcaccagtgagttctttgcctctactctgaccctagacaacctggggaggga ccctgtgcccgcaaaccagacacataggacaaagtttatctataacctggaagacc atgagtggtgtgaaaacatggagtccgttttatagtgactaaaggagggctgaactct gtattagtaatccaagggtcatttttttcttaaaaaaagaaaaaaaggttccaaaaaaa accaaaactcagtacacacacacaggcacagatgcacacacacgcagacagac acaccgactttgtcctttttctcagcatcagagccagacaggattcagaataaggaga gaatgacatcgtgcggcagggtcctggaggccactcgcgcggctgggccacagag tctactttgaaggcacctcatggttttcaggatgctgacagctgcaagcaacaggcact gccaaattcagggaacagtggtggccagcttggaggatggac	28232	NM_013272	SEQ ID NO:48
SPINK1	"serine protease inhibitor, Kazal type 1 / serine protease inhibitor, Kazal type 1"	206239_s_at	+	gagacgtggtaagtgcggtgcagttttcaactgacctctggacgcagaacttcagcca tgaaggtaacaggcatctttcttctcagtgccttggccctgttgagtctatctggtaacact ggagctgactccctgggaagagaggccaaatgttacaatgaacttaatggatgcac caagatatatgaccctgtctgtgggactgatggaaatacttatcccaatgaatgcgtgtt atgttttgaaggtcggaaacgccagacttctatcctcattcaaaaatctgggccttgctg agaaccaaggttttgaaatcccatcaggtcaccgc	6690	NM_003122	SEQ ID NO:49

SPINK 5	"serine protease inhibitor, Kazal type 5 / serine protease inhibitor, Kazal type 5"	205185_at	+	agccatcccatgttagagcttctcaagaggaagacagcccagactctttcagttctctg gattctgagatgtgcaaagactaccgagtattgcccaggataggctatctttgtccaaa ggatttaaagcctgtctgtggtgacgatggccaaacctacaacaatccttgcatgctct gtcatgaaaacctgatacgccaaacaaatacacacatccgcagtacagggaagtgt gaggagagcagcaccccaggaaccaccgcagccagcatgcccccgtctgacga atgacaggaagattgttgaaagccatgagggaaaaaataaaccccagttctgaatc acctaccttcaccatctgtatatacaaagaattcttcggagcttgtcttatttgctatagaa aacaatacagagcttttgggaatggaatcactgattttcagtcttttccatttctttcctccta gaatctgtgatctgagggtataaagacatttccaccaagtttgagccctcaaaatgtcc tgattacaatgctgtctgtcc	11005	NM_006846	SEQ ID NO:50
STC2	stanniocalcin 2	203438_at		gtccacattcctgcaagcattgattgagacatttgcacaatctaaaatgtaagcaaagt agtcattaaaaatacaccctctacttgggctttatactgcatacaaatttactcatgagcc ttcctttgaggaaggatgtggatctccaaataaagatttagtgtttattttgagctctgcatc ttaacaagatgatctgaacacctctcctttgtatcaataaatagccctgttattctgaagt gagaggaccaagtatagtaaaatgctgacatctaaaactaaataaatagaaaaca ccaggccagaactatagtcatactcacacaaagggagaaatttaaactcgaaccaa gcaaaaggcttcacggaaatagcatggaaaaacaatgcttccagtggccacttccta aggaggaacaaccccgtctgatctcagaattggcaccacgtgagcttgctaagtgat aatatctgtttctactacggatttaggcaacaggacctgtacattgtcacattgcat	8614	NM_003714	SEQ ID NO:51
TAZ	transcriptional co-activator with PDZ-binding motif (TAZ)	202132_at		tgggggacttatttgttggggatcttaaataagattccttttgatctaccggaatatacatg tacagagtacattggatcatgttggaaagaaggcaagtgaaaaggtcagagatgaa gtagcgaagttatggaatatcgtggaaaggatactagttgtgaaatggaaagagaca agttatagtaccccaaaagcaaaacaagcaggagatgcaagagatgccccaaaa ggacaaagcaacaattttctgttgccacctttataccggaagactctgttgtagaagaa aagaaggctttggtgcaccttatgtgggaggaggagggggcagggcatgctgatgct gagcgtacaggcagacaagagcgtagcctgctgttgcctccatcactatgaaatgac ttattttacctgaaggacccatggtttatgttcctctaattcctttcactctccctaagccctct gagagagatg	25937	NM_015472	SEQ ID NO:52
TCEA2	"transcription elongation factor A (SII), 2 / transcription elongation factor A (SII), 2"	203919_at		gcctgtcggctcagatcgaggaatgcatcttccgggacgttggaaacacagacatga agtataagaaccgtgtacggagtcgtatctccaacctgaaggatgccaagaaccctg acctgcggcggaatgtgctgtgtggggccataacaccccagcagatcgctgtgatga cctcagaggagatggccagtgatgagctgaaggagatccgtaaggccatgaccaa ggaggccatccgagagcaccagatggcccgcactggcggcacgcagacagacct gttcacctgcggcaagtgcaggaaaaagaactgcacctacacacaggtgcagacc cgcagctctgatgagcccatgaccacctttgttgtctgcaacgagtgtggaaaccgct ggaagttctgctgacccctcgtgtagatgtgctgcagccttgggccctccccggccca cgtcctccgttgacacagcttctctggagaccctagaaggcggcatgtcc	6919	NM_003195 / NM_198723	SEQ ID NO:53

TNNC1	"troponin C, slow / troponin C, slow"	209904_at	+	tggatgacatctacaaggctgcggtagagcagctgacagaagagcagaaaaatgagttcaaggcagccttcgacatcttcgtgctgggcgctgaggatggctgcatcagcaccaaggagctgggcaaggtgatgaggatgctgggccagaaccccacccctgaggagctgcaggagatgatcgatgaggtggacgaggacggcagcggcacggtggactttgatgagttcctggtcatgatggttcggtgcatgaaggacgacagcaaagggaaatctgaggagctgtctgacctcttccgcatgtttgacaaaaatgctgatggctacatcgacctggatgagctgaagataatgctgcaggctacaggcgagaccatcacggaggacgacatcgaggagctcatgaaggacggagacaagaacaacgacggccgcatcgactatgatgagt	7134	NM_003280	SEQ ID NO:54
TRPM2	"transient receptor potential cation channel, subfamily M, member 2"	205708_s_at		acccttggccatcaggcgaggggctgggcctgtgcagctgggcccttggccagagtccactcccttcctggctgtgtcaccccgagcagctcatccaccatggaggtcattggcctgaggcaagttccccggagagtcgggntcccctgtggccccctcaggcctatgtctgtgaggaaggggccctgccactctccccaagagggcctccatgtttcgaggtgcctcaacatggagccttgcctggcctgggctaggggcactgtctgaactcctgactgtcaggataaactccgtgggggtacaggagcccagacaaagcccaggcctgtcaagagacgcagagggcccctgccagggttggccccagggaccctgggacgaggctgcagaagctctccctccctactccctgggagccacgtgctggccatgtggccagggacggcatgagcaggaggcggggacgtgggggccttctggtttggtgtcaacagc	7226	NM_001001188 / NM_003307	SEQ ID NO:55
VAMP4	vesicle-associated membrane protein 4	213480_at		gaagccacaaagatgccacatgttagtatatcagtgagaggtgactccacagtgctctctggagaagcaatatgagtgactgaagagtggggccttttgcttttgcctggatatagggtgctcttctactgtaattgggtgtggaaaaactctggctttatggtattccattaggttcttttcatttaaagtagtcttaaaatcaaagtatccaatattttaaagccacaaagtagattacataattagcagagattttagtcagtaaaatgttagaaatcaaactataagaaaattcaagtcctttattttgtgtcttgggtatatgtcattattttaaattccacactcccttatttaatcactttggtaagtgcctttgatgttttgaaatgtatagtgggagatgagcaaatgtaaatgtcatgtgccctgttccctagcttctcaattcctcataaccattttaccagtgttgcaaagtttagacctttgtgttaatatcagaagtgtatttgtagcccctccatagtgaacaatga	8674	NM_003762 / NM_201994	SEQ ID NO:56
ZNF313	zinc finger protein 313	200868_s_at		gccgaagaagcctgtctgtggggtgtgtcgcagcgctctggcacctggcgtccgagccgtggagctcgagcggcagatcgagagcacagagacttcttgccatggctgccgtaagaatttcttcctgtccaagatccggtcccacgtggctacttgttccaaataccagaattacatcatggaaggtgtgaaggccaccattaaggatgcatctcttcagccaaggaatgtcccaaaccgttacacctttccttgtccttactgtcctgagaagaactttgatcaggaaggacttgtggaacactgcaaattattccatagcacggataccaaatctgtggtttgtccgatatgtgcctcgatgccctggggagaccccaactaccgcagcgccaacttcagagagcacatccagcgccggcaccggttttcttatgacacttttgtggattatgatgttgatgaagaggacatgatgaatcaggtgttgcagcgctccatcatcgaccagtgagcagagtccgtgcttgctatc	55905	NM_018683	SEQ ID NO:57

Table 2: **as described in priority application US60/619027 filed on 18/10/2004.**

Gene Symbol	Gene Title	Affymetrix ID	+ up in *sensitive*	Sequence	Locus Link	RefSeq Transcript ID	SEQ ID NO.
AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1 / alanine-glyoxylate aminotransferase 2-like 1 / alanine-glyoxylate aminotransferase 2-like 1	221008_s_at	+	gctgaaagaagcccacatagaactgcttagggacagcaccactgactccaaagaaaatcccagcagaaagagaaatggaatgtgcacggatacacattcactgctcagtaagaggctcaagacatgactgatttgcattttaaagcaagatgcgatgtccagagttacagagaatgagtagatgtgtctcatcggttaatagctctattatacctctaaaggtggaattgtcagtttagattcataaatgaaaaggtaaatgagtaatcagaataaaccaagtgataatcaaaccatgtcaagattattagttcagactctagcctgttaattttcttagttgatttctgaagctacctgatttattctattaaattgtaagcttgcaaactcaaaataaattggcagatttacctctcatgttttaatgtgtcaaattagagagcaaagtataacaggtgccttcacttttgagactt	64850	NM_031279	SEQ ID NO:58
AKAP12	A kinase (PRKA) anchor protein (gravin) 12 / A kinase (PRKA) anchor protein (gravin) 12	210517_s_at		gtgccatagtgcaggcttggggagctttaagcctcagttatataacccacgaaaaacagagcctcctagatgtaacattcctgatcaaggtacaattctttaaaattcactaatgattgaggtccatatttagtggtactctgaaattggtcactttcctattacacggagtgtgctaaaactaaaaagcattttgaaacatacagaatgttctattgtcattgggaaatttttctttctaacccagtggaggttagaaagaagttatattctggtagcaaattaactttacatcctttttcctacttgttatggttgtttggaccgataagtgtgcttaatcctgaggcaaagtagtgaatatgttttatatgttatgaagaaaagaattgttgtaagtttttgattctactcttatatgctggactgcattcacacatggcatgaaataagtcaggttctttacaaatggtattttgatagatactggattgtgtttgtgccatatttgtgccatt	9590	NM_005100 / NM_144497	SEQ ID NO:59
ANXA6	annexin A6 / annexin A6	200982_s_at		gggatgcatttgtggccattgttcaaagtgtcaagaacaagcctctcttctttgccgacaaactttacaaatccatgaagggtgctggcacagatgagaagactctgaccaggatcatggtatcccgcagtgagattgacctgctcaacatccggagggaattcattgagaaatatgacaagtctctccaccaagccattgagggtgacacctccggagacttcctgaaggccttgctggctctctgtggtggtgaggactagggccacagctttggcgggcacttctgccaagaaatggttatcagcaccagccgccatggccaagcctgattgttccagctccagagactaaggaaggggcaggggtgggggaggggttgggttgggctcttatcttcatggagcttaggaaacgctcccactcccacgggccatcgagggccagcacggctgagcggtgaaaaaccgtagccatagatcctgtcc	309	NM_001155 / NM_004033	SEQ ID NO:60
AREG	amphiregulin (schwannoma-derived growth factor) / amphiregulin (schwannoma-derived growth factor)	205239_at	+	atttcaaaatttctgcattcacggagaatgcaaatatatagagcacctggaagcagtaacatgcaaatgtcagcaagaatatttcggtgaacggtgtggggaaaagtccatgaaaactcacagcatgattgacagtagtttatcaaaaattgcattagcagccatagctgcctttatgtctgctgtgatcctcacagctgttgctgttattacagtccagcttagaagacaatacgtcaggaaatatgaaggagaagctgaggaacgaaagaaacttcgacaagagaatggaaatgtacatgctatagcataactgaagataaaattacaggatatcacattggagtcactgccaagtcatagccataaatgatgagtcggtcctctttccagtggatcataagacaatggaccctttttgttatgatggtttaaactttcaattgtcacttttttatgctatttctgtata	374	NM_001657	SEQ ID NO:61

BCAT1	"branched chain aminotransferase 1, cytosolic / branched chain aminotransferase 1, cytosolic"	214452_at	+	gacaacagccctggaggggaacagagtgagagagatgtttngctctggtaca gcctgtgttgtttgcccagtttctgatatactgtacaaaggcgagacaatacacatt ccaactatggagaatggtcctaagctggcaagccgcatcttgagcaaattaact gatatccagtatggaagagaagagagcgactggacaattgtgctatcctgaatg gaaaatagaggatacaatggaaaatagaggataccaactgtatgctactggga cagactgttgcatttgaattgtgatagatttctttggctacctgtgcataatgtagtttgt agtatcaatgtgttacaagagtgattgtttcttcatgccagagaaaatgaattgcaa tcatcaaatggtgtttcataacttggtagtagtaacttaccttaccttaccnanaaaa atattaatgtaagccatataacatgggattttcctcaannannnnannnnnncct tttgtacttcactcagatacta	586	NM_005504	SEQ ID NO:62
BCL3	B-cell CLL/lymphoma 3 / B-cell CLL/lymphoma 3	204908_s_at	+	gggcagatcttggactcatgaggaggggccccctgcccagaggggtcaacc cttctggaaactgtgaagatctgacttcgccccccccccccccatcttcgggac caggatttgcacagaagcacatgcacctacccatacacccccctcttctgagcgtc cctgttcccccatctcgctccctcccaggactctgaccccagcattctcaggcacc agtccctgtccggaatgccacccacatcttccatttccatgtcccctcccagagct ggtggacccagggaacagccactcccctccactctctaccagataactgagga ggggagaggtgggccgtaacgggcacggatcacgatgtaaattatt	602	NM_005178	SEQ ID NO:63
BST2	bone marrow stromal cell antigen 2 / bone marrow stromal cell antigen 2	201641_at	+	agcttcaggacgcgtctgcagaggtggagcgactgagaagagaaaaccagg tcttaagcgtgagaatcgcggacaagaagtactaccccagctcccaggactcc agctccgctgcggcgccccagctgctgattgtgctgctgggcctcagcgctctgct gcagtgagatcccaggaagctggcacatcttggaaggtccgtcctgctcggcttt tcgcttgaacattcccttgatctcatcagttctgagcgggtcatggggcaacacgg ttagcggggagagcacggggtagccggagaagggcctctggagcaggtctg gaggggccatggggcagtcctgggtgtggggacacagtcgggttgacccagg gctgtctccctccagagcctccctccggacaatgagtccccctcttgtctcccac cctgagattgggcatggggtgcggtgtgggggcatgtgctgcctgttgttatggg ttttttttgcgggggggggttgctttttttctggggtctttgagctccaaa	684	NM_004335	SEQ ID NO:64
C9orf16	chromosome 9 open reading frame 16	204480_s_at	+	catgctggaccagatcaactcctgtctggaccacctggaggagaagaatgacc acctccacgcccgcctccaggagctgctggagtccaaccggcagacacgcct ggagttccagcagcagctcggggaggcccccagtgatgccagcccctaggct ccaagagcccccaaccgggacccaaccctgcctccctgggctaggctctggc ctgggcactcacccccctggcttagacaccttctcaagggctggccttcagggacc cctggtgggtctgcctgcctgggccacccttcctgcctgggcctccccttggccta cctgggccagcccccaccacctggcatgccctcctggggccaagagtgggcct gcaacccacccacttgcctgcccacccaactcctgggcgctccccactctgccc aggccttgagtgtccacattaaatg	79095	NM_024112	SEQ ID NO:65
CAPZA2	"capping protein (actin filament) muscle Z-line, alpha 2"	201237_at		cacttaccagtgagcatatatattttaaaatactttctttggatattgtaattcttaactg gttgtaaattagaaaagctgggattacatatggtgtgcggttacagtctaaattttttc atcctcctatgcatcataagcatgtttgtaatattttcaaaaatagttctactgatgcta caggaatttcaagcctgtggtgaatgttagtatttaccatagggagtgaagtggag ttatggtttcattcaatagagtattgctgattatacttgagtggaatcctttcctcacgt actcccacagacgtctgggcctggaaa	830	NM_006136	SEQ ID NO:66

CCND1	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	208711_s_at		ggcggaggagaacaaacagatcatccgcaaacacgcgcagaccttcgttgcc ctctgtgccacagatgtgaagttcatttccaatccgccctccatggtggcagcggg gagcgtggtggccgcagtgcaaggcctgaacctgaggagccccaacaacttc ctgtcctactaccgcctcacacgcttcctctccagagtgatcaagtgtgacccgga ctgcctccgggcctgccaggagcagatcgaagccctgctggagtcaagcctgc gccaggcccagcagaacatggaccccaaggccgccgaggaggaggaaga ggaggaggaggaggtggacctggcttgcacacccaccgacgtgcgggacgt ggacatctgagggcgccaggcaggcgggcgccaccgccacccgcagcgag ggcggagccggccccaggtgctcccctgacagtccctcctctccggagcattttg ataccagaagggaaagcttcattctccttgttgttggttgtttttttcctttgctctttcccc cttccatctctgacttaagcaaaa	595	NM_001758 / NM_053056	SEQ ID NO:67
CCND1	cyclin D1 (PRAD1: parathyroid adenomatosis 1) / cyclin D1 (PRAD1: parathyroid adenomatosis 1)	208712_at		gttttgggtatgtttaatctgttatgtactagtgttctgtttgttattgttttgttaattacacc ataatgctaatttaaagagactccaaatctcaatgaagccagctcacagtgctgt gtgccccggtcatctagcaagctgccgaaccaaaagaatttgcaccccgctgc gggcccacgtggttggggccctgccctggcagggtcatcctgtgctcggaggcc atctcgggcacaggcccaccccgccccacccctccagaacacggctcacgctt acctcaaccatcctggctgcggcgtctgtctgaaccacgcgggggccttgaggg acgctttgtctgtcgtgatggggcaagggcacaagtcctggatgttgtgtgtatcg agaggccaaaggctggtggcaagtgcacggggcacagcggagtctgtcctgt gacgcgcaagtctgagggtctgggcggcg	595	NM_001758 / NM_053056	SEQ ID NO:68
CDH1	"cadherin 1, type 1, E-cadherin (epithelial)"	201130_s_at		aattcctgccattctggggattcttggaggaattcttgctttgctaattctgattctgctg ctcttgctgtttcttcggaggagagcggtggtcaaagagcccttactgcccccaga ggatgacacccgggacaacgtttattactatgatgaagaaggaggcggagaa gaggaccaggactttgacttgagccagctgcacaggggcctggacgctcggcc tgaagtgactcgtaacgacgttgcaccaaccctcatgagtgtccccggtatcttc cccgccctgccaatcccgatgaaattggaaattttattgatgaaaatctgaaagc ggctgatactgaccccacagccccgccttatgattctctgctcgtgtttgactatga aggaagcggttccgaagctgctagtctgagctccctgaactcctcagagtcaga caaagaccaggactatgactacttgaacgaatggggcaatccgttcaagaagc tggctgacatgtacggaggcg	999	NM_004360	SEQ ID NO:69
CDKN2A	"cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) / cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)"	207039_at	+	cttttcactgtgttggagttttctggagtgagcactcacgccctaagcgcacattcat gtgggcatttcttgcgagcctcgcagcctccggaagctgtcgacttcatgacaag cattttgtgaactagggaagctcaggggggttactggcttctcttgagtcacactgc tagcaaatggca	1029	NM_000077 / NM_058195 / NM_058197	SEQ ID NO:70

CDKN2A	"cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)"	209644_x_at	+	tgaggagccagcgtctagggcagcagccgcttcctagaagaccaggtcatgatgatgggcagcgcccgagtggcggagctgctgctgctccacggcgcggagcccaactgcgccgaccccgccactctcacctgacccgtgcacgacgctgcccgggagggcttcctggacacgctggtggtgctgcaccgggccggggcgcggctggacgtgcgcgatgcctggggccgtctgcccgtggacctggctgaggagctgggccatcgcgatgtcgcacggtacctgcgcgcggctgcgggggcaccagaggcagtaaccatgcccgcatagatgccacggaaggtccctcagacatccccgattgaaagaaccagagaggctctgagaaacctcgggaaacttagatcatcagtcaccgaaggtcctacagggccacaactgcccccgccacaacccaccccgctttcgtagttttcatttagaaaatagagcttttaaaaatgtcctgccttttaacgtagatatatgccttcccc	1029	NM_000077 / NM_058195 / NM_058197	SEQ ID NO:71
CEACAM 7	carcinoembryonic antigen-related cell adhesion molecule 7	206199_at	+	atattagttaccctggtgtgctgtattctctaaaacctttaaatgtttgcatgcagccattcgtcaaatgtcaaatattctctctttggctggaatgacaaaaactcaaataaatgtatgattaggaggacatcataacctatgaatgatggaagtccaaaatgatggtaactgacagtagtgttaatgccttatgtttagtcaaactctcatttaggtgacagcctggtgactccagaatggagccagtcatgctaaatgccatatactcacactgaaacatgaggaagcaggtagatcccagaacagacaaaactttcctaaaaacatgagagtccaggctgtctgagtcagcacagtaagaaagtcctttctgctttaactcttagaaaaaagtaatatgaagtattctgaaattaaccaatcagtttatttaaatcaatttatttatattcttctgttcctggattcccattttacaaaacccactgttctactgttgtattgcccagt	1087	NM_006890	SEQ ID NO:72
CHORDC 1	"cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 / cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1"	218566_s_at		ggatttgtgttcttacagtacttgaaaatatttaaggaagagatgaagctctgcagttttttctatgtgggatgattactttttaaggaggattaattctgaggtagtatagtaactaaaggggaatatatgaattgtttaacaaattagaatttgtttacaactacttgaattttaaattatgtcaaaacttacattacttgccaagcagtatgatgttataggaaacataaataagattacagaggtatcaatttggttaaaattcaccattttataagactaagcaataatcttaacaacctctttcctgaatatttaaatgtgtttgtatggtgttatgactaattgttactgatttagagactaagccctcttaaaacctttagttaaatataaaaagaaattatatatatcttgcctccctgatggaaaactatataaaattgtagacttaaaaggtttgtggaaatacattaggatatcagaaaactaaatatatggagttgctttatgactattacatgt	26973	NM_012124	SEQ ID NO:73
CLU	"clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)"	208791_at	+	ggctgcctgcggatgaaggaccagtgtgacaagtgccgggagatcttgtctgtggactgttccaccaacaacccctcccaggctaagctgcggcgggagctcgacgaatccctccaggtcgctgagaggttgaccaggaaatataacgagctgctaaagtcctaccagtggaagatgctcaacacctcctccttgctggagcagctgaacgagcagtttaactgggtgtcccggctggcaaacctcacgcaaggcgaagaccagtactatctgcgggtcaccacggtggcttcccacacttctgactcggacgttccttccggtgtcactgaggtggtcgtgaagctctttgactctgatcccatcactgtgacggtccctgtagaagtctccaggaagaaccc ta	1191	NM_001831 / NM_203339	SEQ ID NO:74

CLU	"clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) / clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)"	208792_s_at	+	agcagctgaacgagcagtttaactgggtgtcccggctggcaaacctcacgcaaggcgaagaccagtactatctgcgggtcaccacggtggcttcccacacttctgactcggacgttccttccggtgtcactgaggtggtcgtgaagctctttgactctgatcccatcactgtgacggtccctgtagaagtctccaggaagaaccctaaatttatggagaccgtggcggagaaagcgctgcaggaataccgcaaaaagcaccgggaggagtgagatgtggatgttgc	1191	NM_001831 / NM_203339	SEQ ID NO:75
COL4A1	"collagen, type IV, alpha 1"	211980_at		gaaagactgtgctgtcctttaacataggtttttaaagactaggatattgaatgtgaaacatccgttttcattgttcacttctaaaccaaaaattatgtgttgccaaaaccaaacccaggttcatgaatatggtgtctattatagtgaaacatgtactttgagcttattgttttattctgtattaaatattttcagggttttaaacactaatcacaaactgaatgacttgacttcaaaagcaacaaccttaaaggccgtcatttcattagtattcctcattctgcatcctggcttgaaaaacagctctgttgaatcacagtatcagtattttcacacgtaagcacattcgggccatttccgtggtttctcatgagctgtgttcacagacctcagcagggcatcgcatggaccgcaggagggcagattcggaccact	1282	NM_001845	SEQ ID NO:76
COL4A1	"collagen, type IV, alpha 1"	211981_at		tcggctactcttttgtgatgcacaccagcgctggtgcagaaggctctggccaagccctggcgtcccccggctcctgcctggaggagtttagaagtgcgccattcatcgagtgtcacggccgtgggacctgcaattactacgcaaacgcttacagcttttggctcgccaccatagagaggagcgagatgttcaagaagcctacgccgtccaccttgaaggcaggggagctgcgcacgcacgtcagccgctgccaagtctgtatgagaagaacataatgaagcctgactcagctaatgtcacaacatggtgctacttcttcttcttttgttaacagcaacgaaccctagaaatatatcctgtgtacctcactgtccaatatgaaaaccgtaaagtgccttataggaatttgcgtaactaacacaccctgc	1282	NM_001845	SEQ ID NO:77
CTSB	cathepsin B	200838_at		tcccccctgtagactagtgccgtgggagtacctgctgcccagctgctgtggccccctccgtgatccatccatctccagggagcaagacagagacgcaggatggaaagcggagttcctaacaggatgaaagttcccccatcagttcccccagtacctccaagcaagtagctttccacatttgtcacagaaatcagag	1508	NM_001908 / NM_147780 / NM_147781 / NM_147782 / NM_147783	SEQ ID NO:78
CTSB	cathepsin B / cathepsin B	200839_s_at		tggtgttgggagccctttggagaacgccagtctccaggtcccccctgcatctatcgagtttgcaatgtcacaacctctctgatcttgtgctcagcatgattctttaatagaagttttattttcgtgcactctgctaatcatgtgggtgagccagtggaacagcgggagcctgtgctggtttgcagattgcctcctaatgacgcggctcaaaaggaaaccaagtggtcaggagttgtttctgacccactgatctctactaccacaaggaaaatagtttaggagaaaccagcttttactgttt	1508	NM_001908 / NM_147780 / NM_147781 / NM_147782 / NM_147783	SEQ ID NO:79

DAB2	"disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)"	201278_at		ggaaacgttcccagttcattttcagtcctgttgtgagcacagttctgaagggtttattattgtcaaaataagttttgttttgttttgtttatgttgggtttttaatgttgtctcttgacccttaatgctcaggttcttgtgggagttaatcagccacatccaangttaccttgagggggaagaagagggtgatgctcagaagctaaacaagacaggggccacatgaccctctattgattagccccaagtagaaagtcctgtggttttatgtttaatggtaatagttgatcatatatggcataattttctatcagcttcctactcagtcactataaacacagacttgaaatagtactttaaatgtccaaatacctaaatgtgctaaactggaggtaactatttctaggtagttgaatttttgaaagtcatgatcagccacacaactgttttgtacatact	1601	NM_001343	SEQ ID NO:80
DAB2	"disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)"	201280_s_at		aatccttattgttcagagttgtttggggggttctgtttcagagcataaaacctaaaggttatagtagaacaaggcaccttcttaaaagaaatcttgcttcagaccatcagttacagagaatttcctaaagtaaaattgaagcaactacaacttctccttagacactttggaatctaaccacttaaggaccttttaaagagatagcttctcttctttctgaagatcaatttctcccaaggccaagattgtccttttctcccatttcttgctagctattgcaaatgagggaagaacattattcatctctcctccccttttttttctgattctttttcagtcagttttgctcctgggttcaagtagtattaccaccctttcacaagcaacagactc	1601	NM_001343	SEQ ID NO:81
DIAPH2	diaphanous homolog 2 (Drosophila) / diaphanous homolog 2 (Drosophila)	205726_at	+	gctcactacactattcattgcacacaaatgaatttttcactttttaagatgcattcttggtgctcaaaccagatcgaagtttgtctctnaaagctattgtctgcacaggctgctgcatgctctgttgttaaatggatggacaggctattctaaattttggttgatacttttgctactatgggcaattaacttgaaaaaaataatcgatcccaactctgtgctctgatgtacctcttctgccccttttatgacacctttgaccaaatgccttctatggttcacagtgcaggcacaaaactacctctgatacagaaggttctttacaagcttattttacataccgtgaatccctcacctaaagggagaggtgaaagcaaagactgctttgaatgggtattgagggagattgtgtccataccaagccaccctgaagaagtatttcacttgcagtagaactgtggatttgtgctgtcatttcaccttggaataaacacctatctctaagcaggaccaa	1730	NM_006729 / NM_007309	SEQ ID NO:82
EMP1	epithelial membrane protein 1 / epithelial membrane protein 1	201324_at		caccaaattacctaggctgaggttagagagattggccagcaaaaactgtgggaagatgaactttgtcattatgatttcattatcacatgattatagaaggctgtcttagtgcaaaaaacatacttacatttcagacatatccaaagggaatactcacattttgttaagaagttgaactatgactggagtaaaccatgtattcccttatctttactttttttctgtgacatttatgtctcatgtaatttgcattactctggtggattgttctagtactgtattgggcttcttcgttaat	2012	NM_001423	SEQ ID NO:83
EMP1	epithelial membrane protein 1	201325_s_at		ttatcgccctgagaagatctaccccagggagaatctgagacatcttgcctacttttctttattagctttctcctcatccatttcttttatacctttcctttttggggagttgttatgccatgatttttggtatttatgtaaaaggattattactaattctatttctctatgtttattctagttaaggaaatgttgagggcaagccaccaaattacctag	2012	NM_001423	SEQ ID NO:84

EMP1	epithelial membrane protein 1	213895_at		aaggactggtatctttctgtgagcaataaggactggataaagactgcatatccttg tgtcnnnnncagcancnatacaataaggagggttttaatgtgaagcaggcaat ctnccagccccttctggtcttggatgaaatagttgcacagagtattgcaccaana atacacaatggaggctgaaaagttcaacatattttaagtcaattaatcaaattgca ttgattcttgatgctttcttagaggcctacatgatttcttagattgctctgataaactatc ataaggggtccacntcccctcatttagctcccccagggatttcttttcccccatgtca tacacccagtcctaaatcaacccccaaggctatccttccatcccttctgcagagg gaacttttgtcagactctgcaacaaactcctagctctatccagagtgtcctctgctg ctaagattggtatctttctcctcaaaagcctggatggtgaatgggggtgcattagtc agaattctcc	2012	NM_001423	SEQ ID NO:85
EREG	epiregulin / epiregulin	205767_at	+	taaaaacctgtatctgacccactttgtaatttttgctccaatatccattctgtagactttt gaaaaaaaagtttttaatttgatgcccaatatattctgaccgttaaaaaattcttgttc atatgggagaagggggagtaatgacttgtacaaacagtatttctggtgtatatttta atgtttttaaaaagagtaatttcatttaaatatctgttattcaaatttgatgatgttaaat gtaatataatgtattttctttttattttgcactctgtaattgcactttttaagtttgaagagc cattttggtaaacggtttttattaaagatgctatggaacataaagttgtattgcatgca atttaaagtaacttatttgactatgaatattatcggattactgaattgtatcaatttgttt gtgttcaatatcagctttgataattgtgtaccttaag	2069	NM_001432	SEQ ID NO:86
FGF2	fibroblast growth factor 2 (basic)	204421_s_at	+	gggatcctatttagctcttagtaccactaatcaaaagttcggcatgtagctcatgat ctatgctgtttctatgtcgtggaagcaccggatgggggtagtgagcaaatctgccc tgctcagcagtcaccatagcagctgactgaaaatcagcactgcctgagtagtttt gatcagtttaacttgaatcactaactgactgaaaattgaatgggcaaataagtgct tttgtctccagagtatgcgggagacccttccacctcaagatggatatttcttcccca aggatttcaagatgaattgaaatttttaatcaagatagtgtgctttattctgttg	2247	NM_002006	SEQ ID NO:87
FGF2	fibroblast growth factor 2 (basic) / fibroblast growth factor 2 (basic)	204422_s_at	+	atatcttcttcaggctctgacaggcctcctggaaacttccacatatttttcaactgca gtataaagtcagaaaataaagttaacataactttcactaacacacacatatgtag atttcacaaaatccacctataattggtcaaagtggttgagaatatatttttttagtaatt gcatgcaaaatttttctagcttccatcctttctccctcgtttcttctttttttgggggagctg gtaactgatgaaatcttttcccaccttttctcttcaggaaatataagtggttttgtttggt taacgtgatacattctgtatgaatgaaacattggagggaaacatctactgaatttct gtaatttaaaatattttgctgctagttaactatgaacagatagaagaatcttacagat gctgctataaataagtagaaaatataaatttcatcactaaaatatgctattttaaaat ctatttcctatattgtatttctaatcagatgtattactcttattatttctat	2247	NM_002006	SEQ ID NO:88

FLJ22662	hypothetical protein FLJ22662	218454_at	+	gtggctatccactgttagttcagaagctgggcttggactactcttatgatttagctccacgagccaaaattttccggcgtgaccaagggaaagtgactgatacggcatccatgaaatatatcatgcgatacaacaattataagaaggatccttacagtagaggtgaccccctgtaataccatctgctgccgtgaggacctgaactcacctaacccaagtcctggaggttgttatgacacaaaggtggcagatatctacctagcatctcagtacacatcctatgccataagtggtcccacagtacaaggtggcctccctgtttttcgctgggaccgtttcaacaaaactctacatcagggcatgccagaggtctacaactttgattttattaccatgaaaccaattttgaaacttgatataaaatgaaggagggagatgacggactagaagactgtaaataagataccaaaggcactattttagctatgtttttcccatcagaat	79887	NM_024829	SEQ ID NO:89
GADD45 B	"growth arrest and DNA-damage-inducible, beta / growth arrest and DNA-damage-inducible, beta"	207574_s_at		ccccatcacggagggtccagactgtccactcgggggtggagtgagactgactgcaagccccaccctccttgagactggagctgagcgtctgcatacgagagacttggttgaaacttggttggtccttgtctgcaccctcgacaagaccacactttgggacttgggagctggggctgaagttgctctgtacccatgaactcccagtttgcgaattaataagagacaatctattttgttacttgcacttgttattcgaaccactgagagcgagatgg	4616	NM_015675	SEQ ID NO:90
HIF1A	"hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor) / hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)"	200989_at		tcatctgatgtttctatagtcactttgccagctcaaaagaaaacaatacccctatgtagttgtggaagtttatgctaatattgtgtaactgatattaaacctaaatgttctgcctaccctgttggtataaagatattttgagcagactgtaaacaagaaaaaaaaaatcatgcattcttagcaaaattgcctagtatgttaatttgctcaaaatacaatgtttgattttatgcactttgtcgctattaacatcctttttttcatgtagatttcaataattgagtaatttttagaagcattattttaggaatatatagttgtcacagtaaatatcttgtttttctatgtacattgtacaaatttttcattccttttgctctttgtggttggatctaacactaactgt	3091	NM_001530 / NM_181054	SEQ ID NO:91
HOP	homeodomain-only protein / homeodomain-only protein	211597_s_at	+	aagctatgtgtatcttctgtgtaaagcagtggcttcactggaaaaatggtgtggctagcatttccctttgagtcatgatgacagatggtgtgaaaaccatctaagtttgcttttgaccatcacctcccagtagcaatttgctttcataatccatttagcaatccaggcctctgttgaaaagataatatgagggagaagggaacacatttccttctgaacttacttccctaagtcactttccttatgtatcatctaatacaatgatggttgagtgaaaatacagaaggggtgtttgagtattcagatttcataaaacacttccttggaatatagctgcattaacttggaaagaagcctgttgggccagaagacaga	84525	NM_032495 / NM_139211 / NM_139212	SEQ ID NO:92
HOXC10	homeo box C10 / homeo box C10	218959_at		gctggtgtgtgtgtcaaaccctcactcacccacgcactcacacacagcattctgttctccatgcaaagttaagatcgaatccatccgcttgtaggggaaaaaaaggaaaaaaattaaccagagagggtctgtaatctcgcagagcacaggcagaatcgttccttccttgctgcatttcctccttagactaatagacgttttggaaagttcggctagtgttcgtgtgtttgtcgtagcacccagagcctccaccaaaccctctccatgtctttacctcccagtcgctctaagatctgcttgaagtctcgtatttgtactgctttctgcttttctcccaccccctcctagcacccccacatcccccatctagtaacatctcagaaatttcatccagaggaacaaaaaaaattaaaaatagaacatagcaaagcaaagacagaatgccccccccaaatattgtcctgtccctgtctgggagttgtgttatttaaagatattctgtatgttgtatcttttgcatgtagcttccttaat	3226	NM_017409	SEQ ID NO:93

ITGB2	"integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) / integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)"	202803_s_at		atctggaaggctctgatccacctgagcgacctccgggagtacaggcgctttgagaaggagaagctcaagtcccagtggaacaatgataatccccttttcaagagcgccaccacgacggtcatgaaccccaagtttgctgagagttaggagcacttggtgaagacaaggccgtcaggacccaccatgtctgccccatcacgcggccgagacatggcttggccacagctcttgaggatgtcaccaattaaccagaaatccagttattttccgccctcaaaatgacagccatggccggccggtgcttctgggggctcgtcgggggacagctccactctgactggcacagtctttgcatggagacttgaggagggcttgaggttggtgaggttaggtgcgtgtttcctgtgcaagt	3689	NM_000211	SEQ ID NO:94
KHDRBS 3	"KH domain containing, RNA binding, signal transduction associated 3 / KH domain containing, RNA binding, signal transduction associated 3"	209781_s_at		cagcccggccagttggagttgtagtaccacgagggacgccaactcccagaggagtcctgtccacccgagggccagtgagtcggggaagaggacttctcactcccagagcaagaggagtcccccaactgggtacagacctccaccgccacccccgacacaagagacttatggagaatatgactatgatgatggatatggcactgcttatgatgaacagagttatgattcctatgataacagctatagcaccccagcccaaagtggtgctgattactatgattacggacatggactcagtgaggagacttatgattcctacggggcaagaagagtggactaactcaagacacaaggcaccttcagcgaggacagcaaagggcgtctacagagaccagccatatggcagatactgattgtactgtctgatgttgtgaaatagccaatctccaccagtcctgtatactg	10656	NM_006558	SEQ ID NO:95
KRT13	keratin 13 / keratin 13	207935_s_at	+	gagaacacggtggcagagacggagtgccgctatgccctgcagctgcagcagatccagggactcatcagcagcatcgaggcccagctgagcgagctccgcagtgagatggagtgccagaaccaagagtacaagatgctgctggacatcaagacacgtctggagcaggagatcgccacctaccgcagcctgctcgagggccaggacgccaagaagcgtcagccccccgtagcacctctgttaccacgacttctagtgcctctgttaccaccacctctaatgcctctggtcgccgcacttctgatgtccgtaggccttaaatctgcctggcgtcccctccctctgtcttcagcacccagaggaggagagagccggcagttccctgcaggagagaggaggggctgctggacccaaggctcagtccctctgctctcaggacccccctgtcctgactctctcctgatggtgggccctctgtgctcttctcttccggtcggatctctctcctctctgacctggatacgctttggtttctcaacttc	3860	NM_002274 / NM_153490	SEQ ID NO:96
LASS6	LAG1 longevity assurance homolog 6 (S. cerevisiae)	212446_s_at	+	aactttaacttagagcttcattactttaagaatggaaaacaacctctgagtttgatttcccaaagtttcataaagcccctaagctcatgattttcatcaactctttgcccacatagtcatttacctccacagccgtttgttgtcatagaaggggtggtggtgtttggatttgatttttttcaacttgcagtgagaaataggataggtgacaaaaccttacttgttttcttaagacaattcagtgcttgagcatctctgtcagaaatggaatgaaatactgttagccaattagaattattttatgtattgttattgtgttttgctgatttttatatgaaaatataattattcattcttgatctctggaagcaa	25378 2	NM_203463	SEQ ID NO:97

LTBP2	latent transforming growth factor beta binding protein 2 / latent transforming growth factor beta binding protein 2	204682_at		gggagccaaggctttatacgtctaaagaaaatattcagtagctgaatccgccca gtgatagcctgtgggcaccagcagcaagggctgccatgggatacagcaccca tctacaaagacctctattacataaacactgcttcttacaggaaacaaacctcttctg ggatctccttttgtgaaaaccagtttgatgtgctaaaagtaaaaagtctattttccag tgtggtcttgttcagaagcagccagatttccaatgttgtttttcccctccactcagaa acccctgccctttcccttcagaaaacgatggcaggcattcctctgagtttacaagc agagactcactccaacccaaactagctggg	4053	NM_000428 / NM_032035	SEQ ID NO:98
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	203552_at		acacacacatgcaattttgcttaacaaaagtattttataatacagtttcatacagaa ttaccttaaaagggagtcttatgttttcaactacagatagttgtaagggatcntaca gaagatattgatgatagttgaaatattcttagaaggggtgtgtatgtctagctgtgtc taccatgtgtatgtattcttgacaagcagtataaaatacctgtgatttttctttacatta gggataatgcataaggaattaatcttcatatatattatcatccctaatgtagcaggg ggaagtatttaattgcccatgatatgtattttacttatactatgccagagaggaaact ataaagtaattacacatgtaatcttgggtttttcacatatgtaggtattcattttgagta ggttgaagaagaaaaaaaatatttaaatgaattgaattcctgatgggatagtatc aat	11183	NM_006575 / NM_198794	SEQ ID NO:99
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	203553_s_at		gaactctgcatcttcatggtttacagaaattggtgcaggcagccagcagttagatt ccattcatgtaacacagttggagagagataccgttttagtgtgtttagacaaatttgt gaaaattgtaaatctacaaggaaaattaaaatcaagtaagaaactggcctctga gttaagttttgattttcgcattgaatctgtagtatgccttcaagacagtgtgttggctttc tggaaacatgggatgcagggtaaaagcttcaagtcagatgaggttacccagga gatttcagatgaaacaagagttttccgcttattaggatcagacagggttgtcgttttg gaaagtaggccaacagaaaatcctactgcacacagcaatctctacatcttggct ggacatgaaaatagttactaagcaacagaaactgatctcaaatgacaggaaa atgaatatactccattgaaagggaaaataaggaaattcaatacaaactgcacta tgatttgctttaact	11183	NM_006575 / NM_198794	SEQ ID NO:100
MMP2	"matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase) / matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)"	201069_at		ctcagagccacccctaaagagatcctttgatattttcaacgcagccctgctttggg ctgcccctggtgctgccacacttcaggctcttctcctttcacaaccttctgtggctcac agaacccttggagccaatggagactgtctcaagagggcactggtggcccgac agcctggcacagggcagtgggacagggcatggccaggtggccactccagac ccctggcttttcactgctggctgccttagaacctttcttacattagcagtttgctttgtat gcactttgtttttttctttgggtcttgtttttttttccacttagaaattgcatttcctgacaga aggactcaggttgtctgaagtcactgcacagtgcatctcagcccacatagtgatg gttcccctgttcactctacttagcatgtccctaccgagtctcttctccactggatgga ggaaaaccaagccgtggcttcccgctcagccctccctgcccctcccttcaaccat tccccatgggaaat	4313	NM_004530	SEQ ID NO:101

MYC	v-myc myelocytomatosis viral oncogene homolog (avian) / v-myc myelocytomatosis viral oncogene homolog (avian)	202431_s_at	+	gcaacaaccgaaaatgcaccagccccaggtcctcggacaccgaggagaatgtcaagaggcgaacacacaacgtcttggagcgccagaggaggaacgagctaaaacggagcttttttgccctgcgtgaccagatcccggagttggaaaacaatgaaaaggcccccaaggtagttatccttaaaaaagccacagcatacatcctgtccgtccaagcagaggagcaaaagctcatttctgaagaggacttgttgcggaaacgacgagaacagttgaaacacaaacttgaacagctacggaactcttgtgcgtaaggaaaagtaaggaaaacgattccttctaacagaaatgtcctgagcaatcacctatgaacttgtttcaaatgcatgatcaaatgcaacctcacaaccttggctgagtc	4609	NM_002467	SEQ ID NO:102
NRP1	neuropilin 1	210510_s_at		aacatccgcctggtaaccagtcgctctggctgggcacttccacccgcacctcattcctacatcaatgagtggctccaaatagacctgggggaggagaagatcgtgagggcatcatcattcagggtgggaagcaccgagagaacaaggtgttcatgaggaagttcaagatcgggtacagcaacaacggctcggactggaagatgatcatggatgacagcaaacgcaaggcgaagtcttttgagggcaacaacaactatgatacacctgagctgcggacttttccagctctctccacgcgattcatcaggatctaccccgagagagccactcatggcggactggggctcagaatggagctgctgggctgtgaagtggaagcccctacagctggaccgaccactcccaacgggaacttggtggatgaatgtgatgacgaccaggccaactgccacagtggaaca	8829	NM_003873	SEQ ID NO:103
NRP1	neuropilin 1	212298_at		gcaaatatcttaccaggcagcctatgaattaacccaaagaagctttggttggttttggtggatttttatcatgccatgttggacatgagatttttagatcttccttcccacattgctagacgtctcactcaaagacatttgttgggagtcacatttgcatcatagangagacagtccattcatcttagttaaattggattgagaatgccttttgtttccaggaaaatattgatcaccatgaaagaagaatagtttttgtccccagagacattcatttagttgatataatcctaccagaaggaaagcactaagaaacactcgtttgttgtttttaaaggcaacagacttaaagttgtcctcagccaagg	8829	NM_003873	SEQ ID NO:104
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OLFM1	olfactomedin 1	213131_at	+	gcgggccacagacgtcggaagaaactcccgtatttgcagctggaactgcagcccacggcgccccggttttcctccccgccctgtccctctctggtcaaacaacatactaaagaggcgaggcaatgactgttggccagttctcaccggggaaaaacccnactgttaggatggcatgaacatttccttagatcgtggtcagctccgaggaatgtggcnnccaggctctttgangagccatgggctgcacccnggccgtaggcntagtgtaactcgcatcccattgcagtgccngtttcnttgactgtgttgctgtctcttagattaaccgtgctgaggctccnacatagctccntggacctgtgtcntagtacatactgaagcgatggtcagagtgtgtagagtgaagttgctgtgcccacattgtttgaactcgcgtacccccgtagatacattgtgcaacgttcttctgttattcccttgaggtggtaacttcgtatgttcagt	10439	NM_006334 / NM_014279 / NM_058199	SEQ ID NO:106

OSMR	oncostatin M receptor / oncostatin M receptor	205729_at	+	ggagacttgagcttgacctaaggatatgcattaaccactctacagactcccactcagtactgtacagggtggctgtggtcctagaagttcagtttttactgaggaaatatttccattaacagcaattattatattgaaggctttaataaaggccacaggagacattactatagcatagattgtcaaatgtaaatttactgagcgtgttttataaaaaactcacaggtgtttgaggccaaaacagattttagacttaccttgaacggataagaatctatagttcactgacacagtaaaattaactctgtgggtgggggcgggggcatagctctaatctaatatataaaatgtgtgatgaatcaacaagatttccacaattcttctgtcaagcttactacagtgaaagaatgggattggcaagtaacttctgacttactgtcagttgtacttctgctccatagacatcagtattctgccatcatttttgatgactacctcagaacataaaaaggaacgtatatcacataattccagtcacagtttttggttcctctt	9180	NM_003999	SEQ ID NO:107
PCDHAC2	"protocadherin alpha subfamily C, 2 / protocadherin alpha subfamily C, 2"	210674_s_at		ctgacctctttgaagttgcagaatgctttgaaattctaatggtatctgaaatatcagctcatagaaagtaacaaaatttgctgtcaccttaaataagacattttaattttgttataatgtacaatttagaagtttgattaattatattatctatttaggcattaatataaaagaggtaggagtctgttatttaaaaaaagcattaaatttaaaaaaaaactgtcttgtctactttttagcttcattctcccatattttgaagggtgtgtaacttcagctctgcaggattgcatggggtaaaacttgttaccaacacatgtgaaccattgctacattgtaggttgtgatcatttttgccccactgaagcccatgtatctgaccttacgtgccttttgaactaggagaatcgggctaatttattaatgatgataattataatgtatctgtacagcactttttacatttgcgaagtgctttccaatccatgttagttactagttattacagctgtaaggataaaacacgtcatgtggattcattttga	56134	NM_018899 / NM_031883	SEQ ID NO:108
PDGFRA	"platelet-derived growth factor receptor, alpha polypeptide / platelet-derived growth factor receptor, alpha polypeptide"	203131_at		agaaaatttgccaatctttcctactttctatttttatgatgacaatcaaagccggcctgagaaacactatttgtgactttttaaacgattagtgatgtccttaaaatgtggtctgccaatctgtacaaaatggtcctatttttgtgaagagggacataagataaaatgatgttatacatcaatatgtatatatgtatttctatatagacttggagaatactgccaaaacatttatgacaagctgtatcactgccttcgtttatattttttaactgtgataatccccacaggcacattaactgttgcacttttgaatgtccaaaatttatattttagaaataataaaaagaaagatacttacatgttcccaaaacaatggtgtggtgaatgtgtgagaaaaactaacttgatagggtctaccaatacaaaatgtattacgaatgcccctgttcatgtt	5156	NM_006206	SEQ ID NO:109
PDZK1	PDZ domain containing 1 / PDZ domain containing 1	205380_at		gtcaaaccatgactcgcacatggcaaaagaacgggcccacagtacagcctcacattcttcttccaattctgaagatacagagatgtgatgaaaacaagtaatagctttggctgtttatttgatagctgtttctgggtatttaataggaatcctttctcaaggaatgagttgtgacctgtttactgtctctttagaagaaaaactccactggaaaccattcaccatgtgtgactgtcttctgttatcatttgtcttacaggcggctattgcagacggctaatttatgcttaacttaggaagagataaggcaagagctagatttttttcatgtgatcttttccaagcttcaacttaacttaactacatttctctgtatgatgatgtctcttacttctacaggttccttgagcac	5174	NM_002614	SEQ ID NO:110

PEA15	phosphoprotein enriched in astrocytes 15 / phosphoprotein enriched in astrocytes 15	200788_s_at		taaattcacatgcagtctcagagactatttagacaaagttcaagttaggagctttaggatgtgggagtaaaactttaatgggaggggagggctggctgctggaagaaggaagaagccagactggttagacagtactcttaactcctagcccagcctacgtgccctgcccctctggccactgctgcagacacctgccttaacacacacacctctaggactccacagttttgccttaaaggaccttcccaagtctccctttccctgtctggcttctcccttaagaagagagagatacttgtagaattgggtgggggaatgagcatgaactgtccttccatttgggatatgttacattagagtgagagagagaataaggagcctttcttatggaagaaatgggagaagagagacagggttcttttcagcagagtctagtagtttctctgtaaggcaaaataatctaaaaagactaacctgcccacccactccttatattgctgtgagattgcccc	8682	NM_003768 / NM_013287	SEQ ID NO:111
PGM1	phosphoglucomutase 1 / phosphoglucomutase 1	201968_s_at		cggacccatccaagtcatctgattgaagagcatgacagaaacaaaatgtattcaccaagcattttaggatttgactttttcactaaccagttgacgagcagtgcatttacaaggcactgccaaacaagatgcccttgggagctgtgagggaaagaggacctgcgggcttagatcaatctcaattccttttcatgccctcctgcattgctgctgcgtgggtatttgtctccttagccatcaggtacagtttacactacaatgtaagctataggtggagcatcagcagtgagtgaggccattcttcatccttaggatgtggcaatgaaatgatggtgcaagttcctttctcttttgtgaatctttccccccatttcctgtttacatgtaacccaacaaaatgcaatttctagtgccttctgtccaatcagttctttcctctgagtgagacgtacttggctacagatttctgccttgttttgcgacattgtc	5236	NM_002633	SEQ ID NO:112
PI3	"protease inhibitor 3, skin-derived (SKALP)"	203691_at		gattggtatggccttagctcttagccaaacaccttcctgacaccatgagggccagcagcttcttgatcgtggtggtgttcctcatcgctgggacgctggttctagaggcagctgtcacgggagttcctgttaaaggtcaagacactgtcaaaggccgtgttccattcaatggacaagatcccgttaaaggacaagtttcagttaaaggtcaagataaagtcaaagcgcaagagccagtcaaaggtccagtctccactaagcctggctcctgccccattatcttgatccggtgcgccatgttgaatccccctaaccgctgcttgaaagatactgactgcccaggaatcaagaagtgctgtgaaggctcttgcgggatggcctgtttcgttccccagtgaagggagccggtccttgct	5266	NM_002638	SEQ ID NO:113
PLAU	"plasminogen activator, urokinase / plasminogen activator, urokinase"	205479_s_at		cccgaccggtgggcatttgtgaggcccatggttgagaaatgaataatttcccaattaggaagtgtaagcagctgaggtctcttgagggagcttagccaatgtgggagcagcggtttggggagcagagacactaacgacttcagggcagggctctgatattccatgaatgtatcaggaaatatatatgtgtgtgtatgtttgcacacttgttgtgtgggctgtgagtgtaagtgtgagtaagagctggtgtctgattgttaagtctaaatatttccttaaactgtgtggactgtgatgccacacagagtggtctttctggagaggttataggtcactcctggggcctcttgggtcccccacgtgacagtgcctgggaatgtacttattctgcagcatgacctgtgaccagcactgtctcagtttcactttcacatagatgtccctttcttggccagttatcccttccttttagcctagttcatccaatcctcactgggtgggg	5328	NM_002658	SEQ ID NO:114

PLAU	"plasminogen activator, urokinase / plasminogen activator, urokinase"	211668_s_at		accacaacgacattgccttgctgaagatccgttccaaggagggcaggtgtgcgcagccatcccggactatacagaccatctgcctgccctcgatgtataacgatccccagtttggcacaagctgtgagatcactggctttggaaaagagaattctaccgactatctctatccggagcagctgaagatgactgttgtgaagctgatttcccaccgggagtgtcagcagccccactactacggctctgaagtcaccaccaaaatgctgtgtgctgctgacccacagtggaaaacagattcctgccagggagactcaggggggacccctcgtctgttccctccaaggccgcatgactttgactggaattgtgagctggggccgtggatgtgccctgaaggacaagccaggcgtctacacgagagtctcacactt	5328	NM_002658	SEQ ID NO:115
PPIF	peptidylprolyl isomerase F (cyclophilin F) / peptidylprolyl isomerase F (cyclophilin F)	201489_at		gggttgccatccaagtgaaagtcttttccttgaccaaggggggacagtcagttttgcaaaaggactctaatacctgtttaatattgtcttcctaattgggataatttaattaacaagattgactagaagtgaaactgcaacactaacttccccgtgctgtggtgtgacctgagttggtgacacaggccacagaccccagagcttggcttttgaaacacaactcagggcttttgtgaaggttcccccgctgagatctttcctcctggttactgtgaagcctgttggtttgctgctgtcgtttttgaggagggcccatgggggtaggagcagttgaacctgggaacaaacctcacttgagctgtgcctagacaatgtgaattcctgtgttgctaacagaagtggcctgtaagctcctgtgctccggagggaagcatttcctggtaggctttg	10105	NM_005729	SEQ ID NO:116
PPIF	peptidylprolyl isomerase F (cyclophilin F)	201490_s_at		gctgaaggcagatgtcgtcccaaagacagctgagaacttcagagccctgtgcactggtgagaagggcttcggctacaaaggctccaccttccacagggtgatcccttccttcatgtgccaggcgggcgacttcaccaaccacaatggcacaggcgggaagtccatctacggaagccgctttcctgacgagaactttacactgaagcacgtggggccaggtgtcctgtccatggctaatgctggtcctaacaccaacggctcccagttcttcatctgcaccataaagacagactggttggatggcaagcatgttgtgttcggtcacgtcaaagagggcatggacgtcgtgaagaaaatagaatctttcggctctaagagtgggaggacatccaagaagattgtcatcacagactgtggccagttgagctaatctgtggccagggtgctggcatggtggcagctgcaaatgtccatgcacccaggtggccgcgttgggctgtcagccaaggtgcctgaaacgatacgtgtgcccact	10105	NM_005729	SEQ ID NO:117
PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) / prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	204748_at	+	ggttgaatgtttgtccttaggataggcctatgtgctagcccacaaagaatattgtctcattagcctgaatgtgccataagactgaccttttaaaatgttttgagggatctgtggatgcttcgttaatttgttcagccacaatttattgagaaaatattctgtgtcaagcactgtgggttttaatatttttaaatcaaacgctgattacagataatagtatttatataaataattgaaaaaaattttcttttgggaagagggagaaaatgaaataaatatcattaaagataactcaggagaatcttctttacaattttacgtttagaatgtttaaggttaagaaagaaatagtcaatatgcttgtataaaacactgttcactgtttttttaaaaaaaaaacttgatttgttattaacattgatctgctgacaaaacctgggaatttgggttgtgtatgcgaatgtttcagtgcctcagacaaat	5743	NM_000963	SEQ ID NO:118

RRM1	ribonucleotide reductase M1 polypeptide	201476_s_at	+	gaacaagcgtcctggggcatttgctatttacctggagccttggcatttagacatctttgaattccttgatttaaagaagaacacaggaaaggaagagcagcgtgccagagatcttttctttgctctttggattccggatctcttcatgaaacgagtggagactaatcaggactggtctttgatgtgtccaaatgagtgtcctggtctggatgaggtttggggagaggaatttgagaaactatatgcaagttatgagaaacaaggtcgtgtccgcaaagttgtaaaagctcagcagctttggtatgccatcattgagtctcagacggaaacaggcaccccgtatatgctctacaaagattcctgtaatcgaaagagcaaccagcagaacctgggaaccatcaaatgcagcaacctgtgcacagaaatagtggagtacaccagcaaagatgaggttgctgtttgtaatttggcttccctggccctgaatatgtatgt	6240	NM_001033	SEQ ID NO:119
SEMA3B	"sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B / sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B"	203071_at	+	gcccctggagtcgcggagaaagggccgtaaccggaggacccacgcccctgagcctcgcgctgagcgggggccgcgcagcgcaacgcactggtgaccagactgtccccacgccgggaaccaagcaggagacgacaggcgagagaggagccagacagaccctgaaaagaaggacgggttggggccgggcacattgggggtcaccggccgatggagacaccaaccgacaggccctggctgagggcagctgcgcgggcttatttattaacaggataaccttgaatgtagcagccccgggagggcggcacaggtcgggcgcaggattcagccggagggaagggacggggaagccgagctccagagcaacgaccagggccgaggaggtgcctggagtgcccaccctgggagacagaccccacctccttgggtagtgagcagtg	7869	NM_004636	SEQ ID NO:120
SERPINE 1	"serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1"	202627_s_at		ggaactacggggcttacaggagcttttgtgtgcctggtagaaactatttctgttccagtcacattgccatcactcttgtactgcctgccaccgcggaggaggctggtgacaggccnaaaggccagtggaagaaacaccctttcatctcagagtccactgtggcactggccacccctccccagtacaggggtgctgcaggtggcagagtgaatgtcccccatcatgtggcccaactctcctggcctggccatctccctccccagaaacagtgtgcatgggttattttggagtgtaggtgacttgtttactcattgaagcagatttctgcttcctttttatttttataggaatagaggaagaaangtcagatgcgtgcccagctcttcaccccccaatctcttggtggggaggggtgtacctaaatatttatcatatccttgcccttgag	5054	NM_000602	SEQ ID NO:121
SERPINE 1	"serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1"	202628_s_at		aaattgaccatacaatttcatcctccttcaggggatcaaaaggacggagtggggggacagagactcagatgaggacagagtggtttccaatgtgttcaatagatttaggagcagaaatgcaaggggctgcatgacctaccaggacagaactttccccaattacagggtgactcacagccgcattggtgactcacttcaatgtgtcatttccggctgctgtgtgtgagcagtggacacgtgagggggggggtgggtgagagagacaggcagctcggattcaactaccttagataatatttctgaaaacctaccagccagagggta	5054	NM_000602	SEQ ID NO:122
SLC20A1	"solute carrier family 20 (phosphate transporter), member 1 / solute carrier family 20 (phosphate transporter), member 1"	201920_at		gtatcaggcttcaattccattatgttttaatgttgtctctgaagatgacttgtgattttttttctttttttaaaccatgaagagccgtttgacagagcatgctctgcgttgttggtttcaccagcttctgccctcacatgcacagggatttaacaacaaaaatataactacaacttcccttgtagtctcttatataagtagagtccttggtactctgccctcctgtcagtagtggcaggatctattggcatattcgggagcttcttagagggatgaggttctttgaacacagtgaaaatttaaattagtaactttttttgcaagcagtttattgactgttattgctaagaagaagtaagaaagaaaaagcctgttggcaatcttggttatttctttaagatttctggcagtgtgggatggatgaatgaagtggaatgtgaactttgggcaagttaaatgggacagccttccatgttcatttgtctacctcttaactga	6574	NM_005415	SEQ ID NO:123

SPRY1	"sprouty homolog 1, antagonist of FGF signaling (Drosophila)"	212558_at		taattttagattcgccttacaatgtaaatcttcacattggagataatattggttggaccttgcccatcttcactctagccttcgtatttgtgaaggactcagccaccttccttcttcaccccatgcttctcaccaaatttttgttgtcattgagggcacttggataactcaagttgatatttatagctgatcaatctatatgtgtcacagaactatgctgcctaaagtgatcttggctccttaatggtccttttggccccttggatagttaacagctgagtaattctaatctcttctgtgttttccttgccttaaccacaaattgtgg	10252	NM_005841 / NM_199327	SEQ ID NO:124
SPRY2	sprouty homolog 2 (Drosophila) / sprouty homolog 2 (Drosophila)	204011_at		gagatacagaacttggtgacccatgtattgcataagctaaagcaacacagacactcctaggcaaagtttttgtttgtgaatagtacttgcaaaacttgtaaattagcagatgactttttccattgttttctccagagagaatgtgctatatttttgtatatacaataatatttgcaactgtgaaaaacaagttgtgccatactacatggcacagacacaaaatattatactaatatgttgtacattcggaagaatgtgaatcaatcagtatgtttttagattgtattttgccttacagaaagcctttattgtaagactctgatttccctttggacttcatgtatattgtacagttacagtaaaattcaacctttattttctaatttttcaacatattgtttagtgtaaagaatatttatttgaagttttattattttataaaaaagaatatttattttaagaggcatcttacaaattttgccccttt	10253	NM_005842	SEQ ID NO:125
SRPUL	sushi-repeat protein / sushi-repeat protein	205499_at		gcggcatgtgaccatcattgaactggtgggacagccacctcaggaggtggggcgcatccgggagcaacagctgtcagccaacatcatcgaggagctcaggcaatttcagcgcctcactcgctcctacttcaacatggtgttgattgacaagcagggtattgaccgagaccgctacatggaacctgtcacccccgaggaaatcttcacattcattgatgactacctactgagcaatcaggagttgacccagcgtcgggagcaaagggacatatgcgagtgaacttgagccagggcatggttaaagtcaagggaaaagctcctctagttagctgaaactgggacctaataaaaggaggaaatgttttcccacagttctagggacaggactctgaggtgggtgagtttgacaaatcctgcagtgtttccaggcatcctttaggactgtgtaatagtttccctagaagctaggtagggactgaggacaggccttgggcagtgggtt	27286	NM_014467	SEQ ID NO:126
TCF8	transcription factor 8 (represses interleukin 2 expression) / transcription factor 8 (represses interleukin 2 expression) / transcription factor 8 (represses interleukin 2 expression)	208078_s_at	+	agactgggcgaaaggctgtccggagggcagaccaggtgccttgccgcagagaaaacaccaaagtctcctgttcgctcataaagaagtttttgggatgggagagaatccagaccatcttggggcagccaggccccttgccttcatttttacagaggtagcacaactgattccaacacaaaaccccttccccttttttaaaatgatttctgttctaatgccatagatcaaaggcctcagaaaccattgtgtgtttcctctttgaagcaatgacaagcactttactttcacggtggtttttgtttttcttattgctgtggaacctcttttggaggacgttaaaggcgtgttttacttgtttttttaagagtgtgtgatgtgtgttttgtagatttcttgacagtgctgtaatacagacggcaatgcaatagcctatttaa	6935	NM_030751	SEQ ID NO:127
TGFA	"transforming growth factor, alpha / transforming growth factor, alpha"	205016_at		cctgccctctagttggttctgggctttgatctcttccaacctgcccagtcacagaaggaggaatgactcaaatgcccaaaaccaagaacacattgcagaagtaagacaaacatgtatatttttaaatgttctaacataagacctgttctctctagccattgatttaccaggctttctgaaagatctagtggttcacacagagagagagagagagtactgaaaaagcaactcctcttcttagtcttaataatttactaaaatggtcaacttttcattatctttattataataaacctgatgcttttttttagaactccttactctgatgtctgtatatgttgcactgaaaaggttaatatttaatgttttaatttattttgtgtggtaagttaattttgatttctgtaatgtgttaatgtgattagcagttattttccttaatatctgaattatacttaaagagtagtgagcaatataagacgcaattgtgtttttcagt	7039	NM_003236	SEQ ID NO:128

TGFBR2	"transforming growth factor, beta receptor II (70/80kDa) / transforming growth factor, beta receptor II (70/80kDa)"	208944_at		gtttggatggtggaaggtctcattttattgagatttttaagatacatgcaaaggtttgg aaatagaacctctaggcaccctcctcagtgtgggtgggctgagagttaaagaca gtgtggctgcagtagcatagaggcgcctagaaattccacttgcaccgtagggca tgctgataccatcccaatagctgttgcccattgacctctagtggtgagtttctagaat actggtccattcatgagatattcaagattcaagagtattctcacttctgggttatcag cataaactggaatgtagtgtcagaggatactgtggctt	7048	NM_003242	SEQ ID NO:129
TIEG	TGFB inducible early growth response / TGFB inducible early growth response	202393_s_at		tttgcctgcagtttcttgtgtagatttgaaaattgtataccaatgtgttttctgtagactct aagatacactgcactttgtttagaaaaaaaactgaagatgaaatatatattgtaa agaagggatattaagaatcttagataacttcttgaaaaagatggcttatgtcatca gtaaagtacctttatgttatgaggatataatgtgtgctttattgaattagaaaattagt gaccattattcacaggtggacaaatgttgtcctgttaatttataggagtttttttggga tgtggaggtagttgggtagaaaaattattagaacattcactttgttaacagtatttct cttttattctgttatatagtggatgatatacacagtggcaaaacaaaagtacattgct taaaatatatagtgaaaaatgtcactatatcttcccatttaacattgtttttgtatattgg gtgtagatttctgacatcaaaacttggacccttggaaaacaaaagttttaattaaa aaaaatccttgtgacttacaatttgcac	7071	NM_005655	SEQ ID NO:130
TIMP3	"tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)"	201147_s_at		gagtcggagatgatgcagcacacacacaattccccagcccagtgatgcttgtgt tgaccagatgttcctgagtctggagcaagcacccaggccagaataacagagct ttcttagttggtgaagacttaaacatctgcctgaggtcaggaggcaatttgcctgcc ttgtacaaaagctcaggtgaaagactgagatgaatgtctttcctctccctgcctccc accagacttcctcctggaaaacgctttggtagatttggccaggagctttcttttatgt aaattggataaatacacacaccatacactatccacagatatagccaagtagattt gggtagaggatactatttccagaatagtgtttagctcacctagggggatatgtttgt atacacatttgcatatacccacatgggg	7078	NM_000362	SEQ ID NO:131
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TIMP3	"tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) / tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)"	201149_s_at		aggggctgaactatcggtatcacctgggttgtaactgcaagatcaagtcctgcta ctacctgccttgctttgtgacttccaagaacgagtgtctctggaccgacatgctctc caatttcggttaccctggctaccagtccaaacactacgcctgcatccggcagaa gggcggctactgcagctggtaccgaggatgggcccccccggataaaagcatc atcaatgccacagacccctgagcgccagaccctgccccacctcacttccctccc ttcccgctgagcttcccttggacactaactcttcccagatgatgacaatgaaattag tgcctgttttcttgcaaatttagcacttggaacatttaaagaaaggtctatgctgtcat atggggtttattgggaactatcctcctggcc	7078	NM_000362	SEQ ID NO:133

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TNFRSF6	"tumor necrosis factor receptor superfamily, member 6"	215719_x_at	+	accaaggttctcatgaatctccaaccttaaatcctgaaacagtggcaataaatttatctgatgttgacttgagtaaatatatcaccactattgctggagtcatgacactaagtcaagttaaaggctttgttcgaaagaatggtgtcaatgaagccaaaatagatgagatcaagaatgacaatgtccaagacacagcagaacagaaagttcaactgcttcgtaattggcatcaacttcatggaaagaaagaagcgtatgacacattgattaaagatctcaaaaaagccaatctttgtactcttgcagagaaaattcagactatcatcctcaaggacattactagtgactcagaaaattcaaacttcagaaatgaaatccaaagcttggtctagagtgaaaaacaacaaattcagttctgagtatatgcaattagtgtttganaagattcttaatagctggctgtaaatactgcttggttt	355	NM_000043 / NM_152871 / NM_152872 / NM_152873 / NM_152874 / NM_152875 / NM_152876 / NM_152877	SEQ ID NO:136
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TNFSF10	"tumor necrosis factor (ligand) superfamily, member 10 / tumor necrosis factor (ligand) superfamily, member 10"	202688_at	+	ctctacctcatatcagtttgctagcagaaatctagaagactgtcagcttccaaacattaatgcaatggttaacatcttctgtctttataatctactccttgtaaagactgtagaagaaagcgcaacaatccatctctcaagtagtgtatcacagtagtagcctccaggtttccttaagggacaacatccttaagtcaaaagagagaagaggcaccactaaaagatcgcagtttgcctggtgcagtggc	8743	NM_003810	SEQ ID NO:138

TUBB4	"tubulin, beta, 4"	213476_x_at		gctcacccagcagatgttcgatgccaagaacatgatggccgcctgcgacccgcgccacggccgnctanctgacggtggccaccgtgttccggggccgcatgtccatgaaggaggtggacgagcagatgctggccatccagagcaagaacagcagctacttcgtggagtggatccccaacaacgtgaaggtggccgtgtgtgacatcccgccccgcggcctcaagatgtcctccaccttcatcgggaacagcacggccatccaggagctgttcaagcgcatctccgagcagttcacggccatgttccggcgcaaggccttcctgcactggtacacgggcgagggcatggacgagatggagttcaccgaggccgagagcaacatgaacgacctggtgtccgagtacc	10381	NM_006086	SEQ ID NO:139
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TUSC3	tumor suppressor candidate 3	209228_x_at		acccaactactctggtaccattgctttggccctgttagtgtcgcttgttggaggtttgctttatttgagaaggaacaacttggagttcatctataacaagactggttgggccatggtgtctctgtgtatagtctttgctatgacttctggccagatgtggaaccatatccgtggacctccatatgctcataagaacccacacaatggacaagtgagctacattcatgggagcagccaggctcagtttgtggcagaatcacacattattctggtactgaatgccgctatcaccatggggatggttcttctaaatgaagcagcaacttcgaaaggcgatgttggaaaaagacggataatttgcctagtgggattgggcctggtggtcttcttcttcagttttctactttcaatatttcgttccaagtaccacggctatccttatagtgatctggactttgagtgagaagatgtgatttggaccatggcacttaaaaactctataacctcagcctttaat	7991	NM_006765 / NM_178234	SEQ ID NO:141
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Example 4

RT-PCR Confirmation Studies

In addition, the sequence of the RT-PCR primers used in the confirmatory follow up studies as highlighted in Figs 3, 4, 5 and 6 are listed in Table 3. Note that DAPK2 was not identified by Affymetrix analysis, only via follow up of the DAPK gene family by RT-PCR following discovery of predictivity of DAPK1. Hence no Affymetrix ID or Affymetrix ID sequence is provided for DAPK2.

Table 3

Sequences relevant to genes followed up by RT-PCR (see Figs 3, 4, 5 & 6)
(all sequences written 5'-3')

Gene	affy id	affy probe seq	Taqman Forward Primer	Taqman Reverse Primer	Taqman probe
EMP1	201324_at	CACCAAATTACCTAGGCTGAGGTTAGAGAGATTGGCCAGCAAAAACTGTGGGAAGATGAACTTTGTCATTATGATTTCATTTATCACATGATTATAGAAGGCTGTCTTAGTGCAAAAAACATACTTACATTTCAGACATATCCAAAGGGAATACTCACATTTTTGTTAAGAAGTTGAACTATGACTGGAGTAAACCATGTATTCCCTTATCTTTTACTTTTTTTCTGTGACATTTATGTCCTCATGTAATTTGCATTACTCTGGTGGATTGTTCTAGTACTGTATTGGGCTTCTTCGTTAAT	AGCCATCCTGCCCTTCTGA	ACCTTACAAACTCTCTTTCC	CAAAGCAAAACATCACATTCCAGTC
NES	218678_at	GCAGCACTCTTAACTTACGATCTCTTGACATACGGTTTCTGGCTGAGAGGCCTGGCCCGCTAAGGTGAAAAGGGGTGTGGGCAAAGGAGCCTACTCCAAGAATGGAGGCTGTAGGAATATAACCTCCCACCCTGCAAAGGGAATCTCTTGCCTGCTCCATTCTCATAGGCTAAGTCAGCTGAATCCCGATAGTACTAGGTCCCCTTCCCTCCGCATCCCGTCAGCTGGAAAAGGCCTGTGGGCCCAGAGGCTTCTCCAAAGGGAGGGTGACATGCTGGCTTTTGTGCCCAAGCTCACCAGCCCTGCGCCACCTCACTGCAAGTAGTGCACCATCTCACTGCAGTAGCACGCCCTCCTGGGCCGTCTGGCCTGTGGCTAATGGAGGTGACGGCACTCCCATTGTGCTGACTCCCCCCATCCCTGCCACGCTGTGGCCCTGCCTGGCTAGTCCCTGCCTGAATAAAG	GCCCCTTTCAGGAGGAGGA	AGTGCCGGGGAGATGGTCTT	AGTGCTCTGAAGACCTCTTGGGC
DAPK1	203139_at	CCTCCTCCAGGGTGATTTTATGATCAGTGTTGTTGCTCTAGGAAGACATTTTTCCGTTTGCTTTTGTTCCAATGTCAATGGTGAACGTCCACATGAAACCTACACACTGTCATGCTTCATCATTCCCTCTCATCTCAGGTAGAAGGTTGACACAGTTGTAAGGGTTACAGAGACCTATGTAAGAATTCAGAAGACCCCTGACTCATCATTTGTGGCAGTCCCTTATAATTGGTGCATAGCCAGATGGTTTCCACATTTAGATCCTGGTTTCATAACTTCCTGTACTTGAAGTCTAAAAGCAGAAAATAAAGGAAGCAAGTTTTTCTTCCATGATTTTAAATTGTGATCGAGTTTTAAATTGATAGGAGGGAACATGTCCTAATTCTTCTGTCCTGAGAA	AGGAAACGCTACCTCTCTGT	CTGGAGGAGGATTCCCTTCT	CTTGCTGTATGCTGATCATCGCC
DAPK2	Not applicable	Not applicable	GGGTAGGCACCTGGCATC	AGTGCAGTGGCGTGATCTC	TACTCCAGGGGCTGAGGTGACA

Example 5

Diagnostic test for Clinical Studies

The predictive gene lists above have been generated using the preclinical studies described. The following approach is employed to develop a diagnostic test for the clinical setting based on this data.

a) Identify patients which represent the population of individuals whom we would expect to derive benefit from a diagnostic test, and for which pre-treatment tumour samples and outcome of gefitinib treatment are known or will be available. For each sample the expression level for our genes of interest is evaluated, using for example the RNA signal from RT-PCR. QC procedures are applied to identify the set of samples and genes to take forward to step b).

a) Identify a subset of the genes which together are able to distinguish between patients showing different responses to gefitinib. There are a variety of methods which are useful to select the subset of genes and combine their expression values to provide a prediction, possibly a predictive value and a corresponding threshold which distinguishes between different patient groups. An example is stepwise Linear Discriminant Analysis where genes that distinguish well between patient groups are successively added to a linear combination until addition of a further gene does not provide additional predictive power (Mardia et al.). The threshold value of the linear combination is then selected to give the appropriate sensitivity and specificity properties.

d) Tool validation would partly be carried out during development in step 2, for example using cross validation and permutation tests. In addition, the finally developed diagnostic procedure (gene subset and method of combining to generate a prediction and a platform for biological analysis) is tested and validated in its entirety using an independent set of samples not used within tool development in step b).

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CLAIMS

1. A method of selecting a mammal having or suspected of having a tumour for treatment with an erbB receptor drug which comprises testing a biological sample from the mammal for expression of any one of the genes listed in Table 1 or DAPK2, whereby to predict an increased likelihood of response to the erbB receptor drug.

2. A method according to claim 1 comprising testing a biological sample from the mammal for expression of any one of NPAS2, NES, CHST7, DAPK1, ACOX2, GSPT2, TNNC1 or DAPK2.

3. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of any one of NPAS2, NES, CHST7 or DAPK1.

4. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of at least two of NPAS2, NES, CHST7 or DAPK1.

5. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of at least three of NPAS2, NES, CHST7 or DAPK1.

6. A method according to any preceding claim comprising testing a biological sample from the mammal for expression of NPAS2, NES, CHST7 and DAPK1.

7. A method according to any preceding claims additionally comprising testing a biological sample from the mammal for expression of any gene listed in Table 2 as defined herein.

8. A method according to claim 7 comprising testing a biological sample from the mammal for expression of any one of EMP1, SLC20A1, SPRY2 or PGM1.

9. A method according to any one of claims 7-8 comprising testing a biological sample from the mammal for expression of EMP1.

10. A method according to any preceding claim wherein the tumour is selected from the group consisting of leukaemia, multiple myeloma, lymphoma, bile duct, bone, bladder, brain, CNS, glioblastoma, breast, colorectal, cervical, endometrial, gastric, head, neck, hepatic, lung, muscle, neuronal, oesophageal, ovarian, pancreatic, pleural membrane, peritoneal membrane, prostate, renal, skin, testicular, thyroid, uterine and vulval.

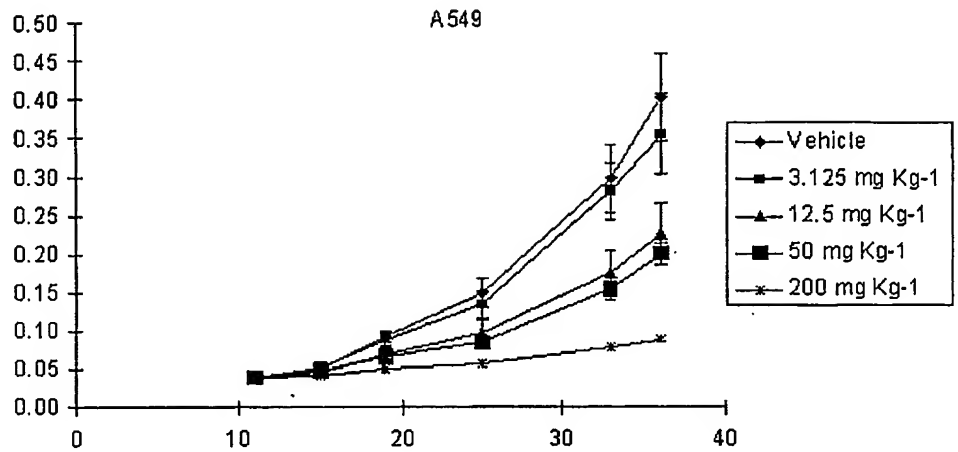
11. A method according to claim 10 wherein the tumour is selected from one of non-small cell lung, pancreatic, head or neck.

12. A method according to any preceding claim wherein the erbB receptor drug is selected from any one of gefitinib, erlotinib, PKI-166, EKB-569, HKI-272, lapatinib, canertinib, AEE788, XL647, BMS 5599626, cetuximab, matuzumab, panitumumab, MR1-1, IMC-11F8 or EGFRL11.

13. A method according to claim 12 wherein the erbB receptor drug is gefitinib.

14. A method according to any preceding claim wherein the mammal is a human and in which the method comprises testing a biological sample from the human for increased expression of DAPK1 and decreased expression of NPAS2, NES, CHST7 and EMP1 whereby to predict an increased likelihood of response to gefitinib.

Figure 1



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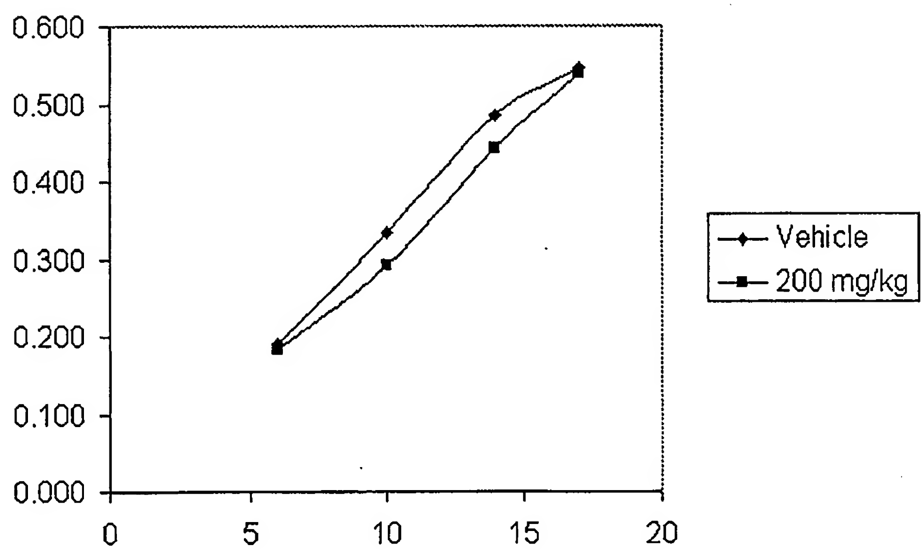

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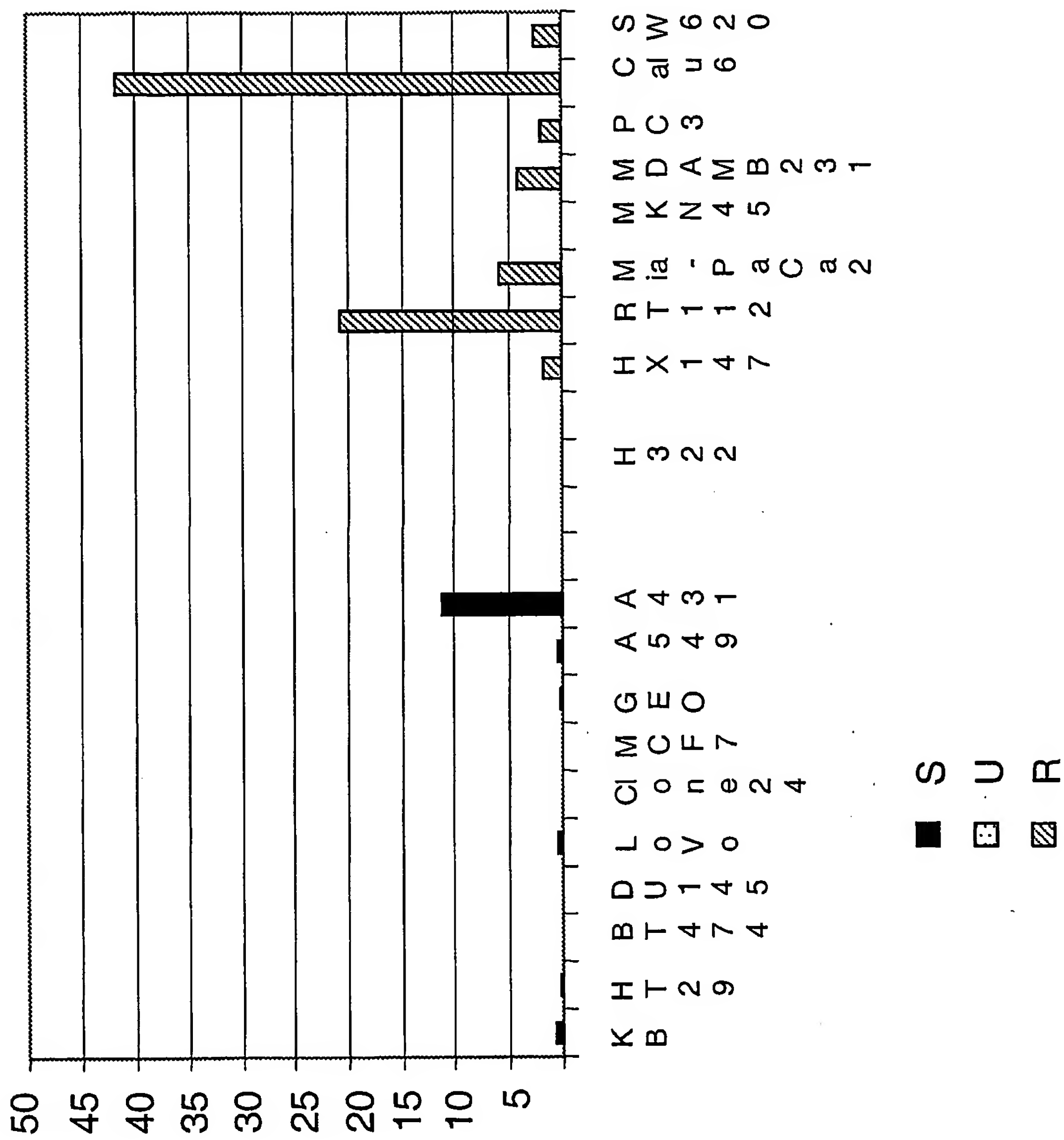
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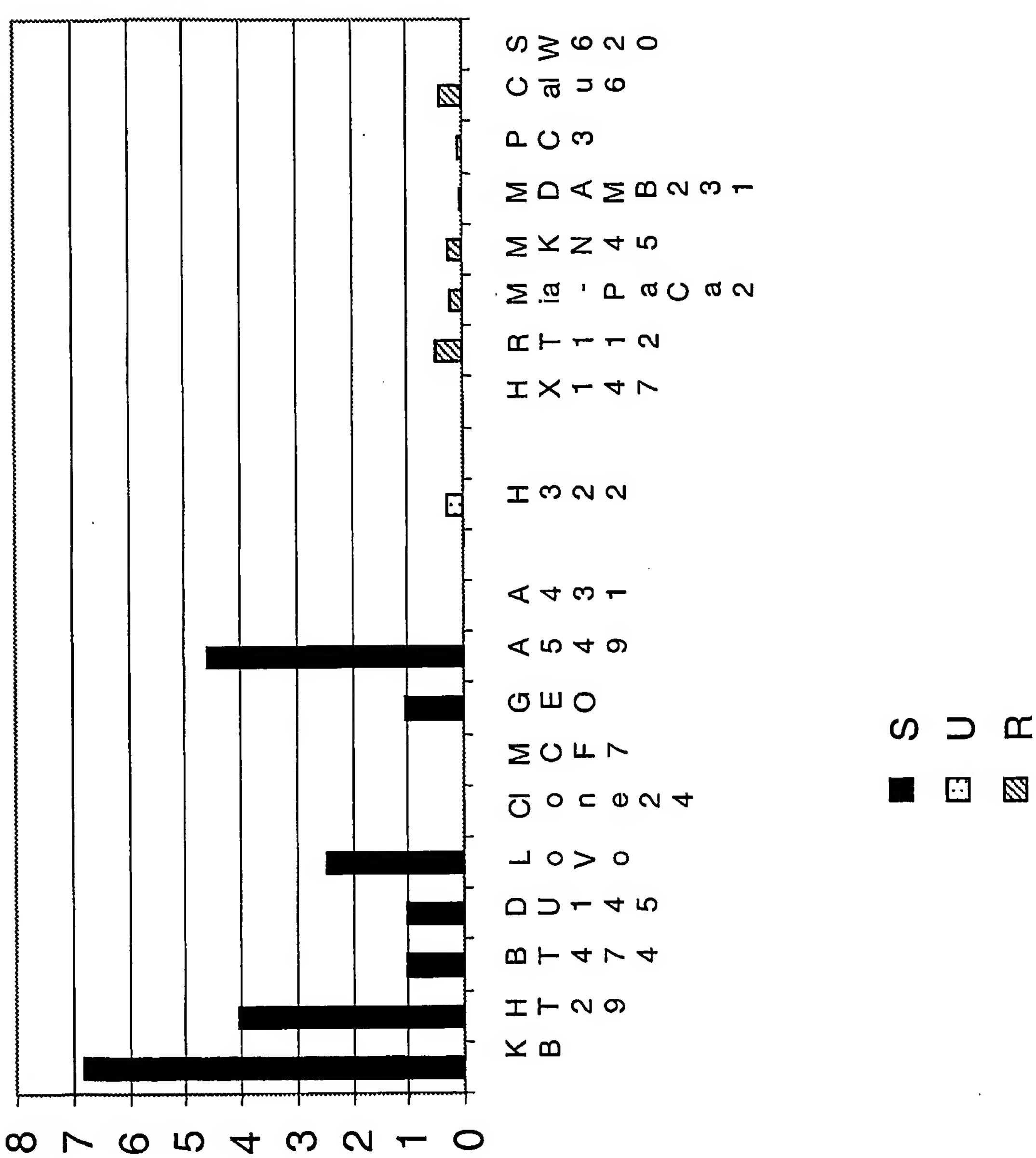
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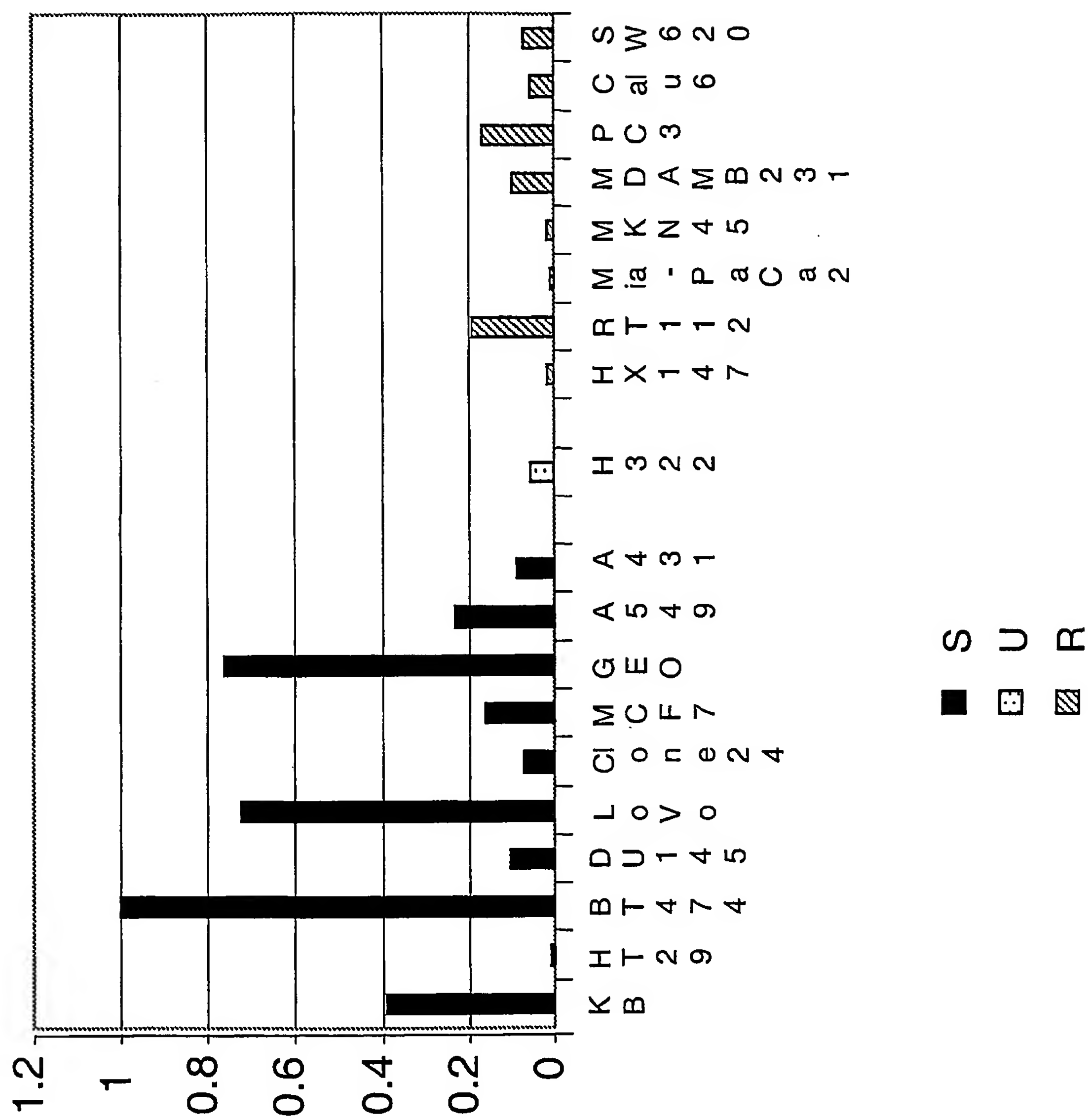
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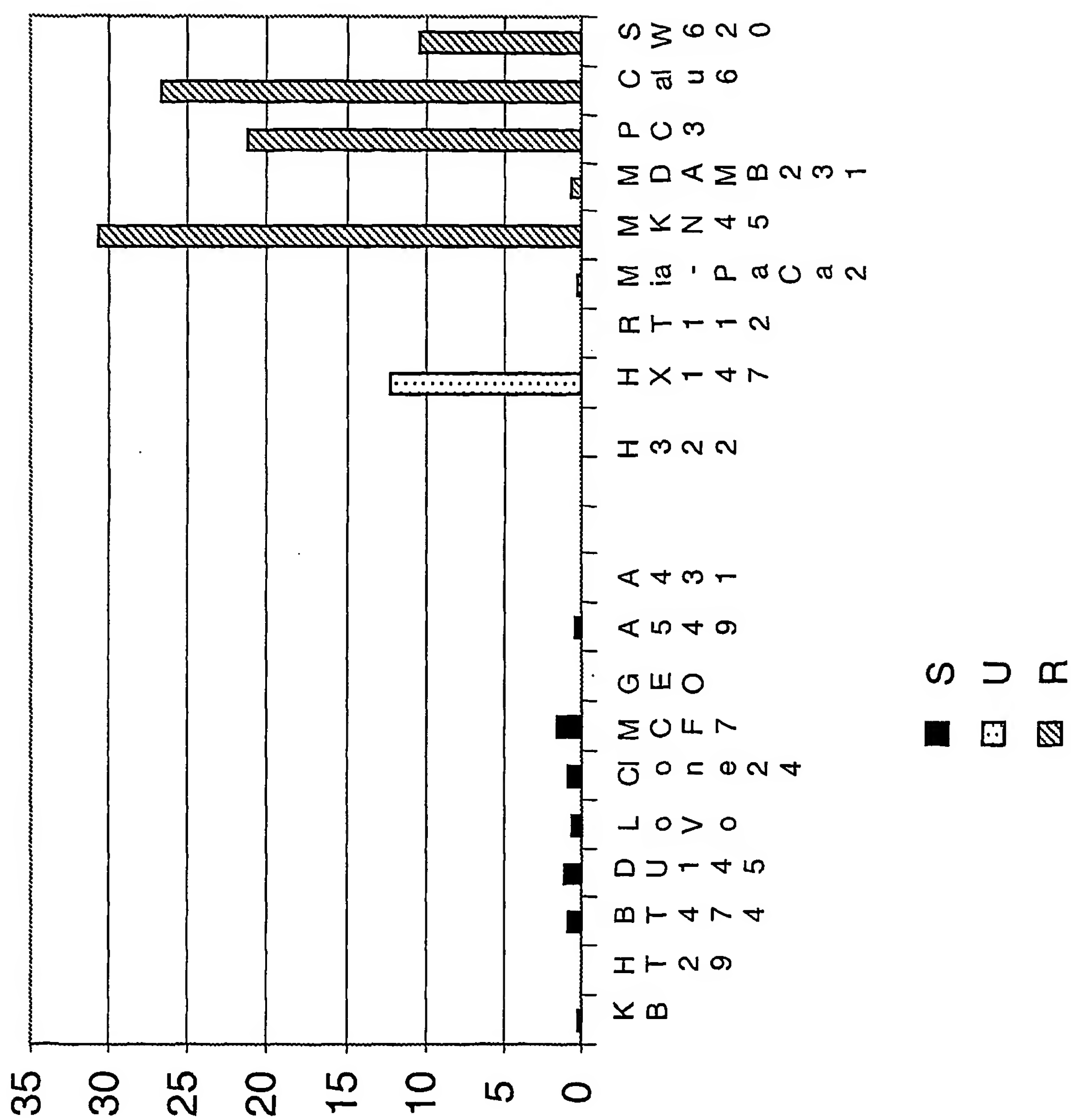
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gcatggtcag ggtcccagct gtaggtgaga gcagggcact gtccagctgt ccactgggga 180

agtcaagatg tcctaaggcc caggtcaggg catctggagt ctgaaggacc ctagttccta 240

gaggcatctg gcagcaagaa ggtgaggcat cagggaacgg gaatcaggct gggactgatc 300

agaggtgaag ggacagagag aggagaggag gaagattgag ctgggggcaa cagccaagct 360

cacctgggca ggtctctgcc acctccttgc tctgtgagct gtcagtctag gttattctct 420

tttttgtgg ctatttttaa ttgctttgga tttgttaaat gttttctgtc ttctgttaag 480

tgtgttt 487

<210> 5
<211> 318
<212> DNA
<213> Homo Sapiens

<400> 5
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aacccctcag catactggga atctcttcct gaacaacgaa tgtaaatttg gtcaagtcta 120

ctcttccgtt cattcaatta ttttaagcat ttgaattatt tattgtatat cctaaatata 180

tttctccttt ggcagtgact agatttccac taatgtgtct taatctatcc ctccagctgg 240

cagttactgt ttttttaatc ccctgaagtt gtcctgtagg agacagaaat tctttgctgt 300

ctgtatccct tggagtaa 318

<210> 6
<211> 135
<212> DNA
<213> Homo Sapiens

<400> 6
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acacacattg aaaat 135

<210> 7

<211> 402
<212> DNA
<213> Homo Sapiens

<400> 7
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cgatttgaat ataacctgcc gctttgcagg tgtattccac gtggagaaaa atggtcgcta 120

cagcatctct cggacggagg ccgctgacct ctgcaaggct ttcaatagca ccttgcccac 180

aatggcccag atggagaaag ctctgagcat cggatttgag acctgcagtt tgcattgcag 240

tcaacagtcg aagaaggtgt gggcagaaga aaaagctagt gatcaacagt ggcaatggag 300

ctgtggagga cagaaagcca agtggactca acggagaggc cagcaagtct caggaaatgg 360

tgcatttggt gaacaaggag tcgtcagaaa ctccagacca gt 402

<210> 8
<211> 417
<212> DNA
<213> Homo Sapiens

<400> 8
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aaaagagaca aaagacatct tcgaatccat atttcaagcc tggtagaatt ggcttttcta 120

gcagaacctt tccaaaagtt ttatattgag attcataaca acaccaagaa ttgattttgt 180

agccaacatt cattcaatac tgttatatca gaggagtagg agagaggaaa catttgactt 240

atctggaaaa gcaaaatgta cttaagaata agaataacat ggtccattca cctttatgtt 300

atagatatgt ctttgtgtaa atcatttgtt ttgagttttc aaagaatagc ccattgttca 360

ttcttgtgct gtacaatgac cactgttatt gttactttga cttttcagag cacaccc 417

<210> 9
<211> 546
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (104)..(104)
<223> n is a, c, g, or t

<400> 9
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ttcaccttca tcgcagactg aaagtttcag tttttatttt tttncagaaa gcacgaaaaa 120

ttatttataa tagtctggag aaaaaacaca ctgtaatatt tcaagtgtat gcagtagaat 180

gtactgtaac tgagcccttt cccacatgtc taggctccaa tgtctcctgt aggtccacct 240

aactgtgtgt tttcagggac aatgccatcc atgtttgtgc tgtagacttg ctgctgctga 300

atcctttctg ggactttct catcgggcag ggagcagagg gcttctcgtt catgcaccct 360

ttgcctgaac acccatgtag ctgctgtgtt gtgtatatat tactcttaag aggagtgtgt 420

gtgtctgtgt ttgttttaaa agtcacttat ttcttacagt gatttcaatt gcaccatgac 480

ttcttcacta aaaccacaaa gtcctgctta aaactatgga aaacctaacc tgattagagc 540

cttgac 546

<210> 10
<211> 546
<212> DNA
<213> Homo Sapiens

<400> 10
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ttctgctgag caggaatatc atgagctgtt caataatgac ggacgcattg gttgagatga 120

agtttccagt aaggaagtga cagtgcaatg tggatattta tggctgtaaa ataggaagag 180

ctttagttcc caggctgaac ctgccactgc tggagccatt tcaacaaggc atcctcacaa 240

caaagaagag atgtgatttg gtaccatttc acaccagcag gtgtctggac gaaaacatca 300

atgtgaataa gggccaagtg cagtcctgtc ttgattaaat tacttaataa tattattaaa 360

taataatagg tctgggcagt attgtttta acctgactca tccagctgtc cttcaaatag 420

ctccgtctcc ctctacccag aactgatttt taaaaagaag taatttttct ccctgggctg 480

ggaaaaccct aatgaactga aacacacttt tactttaaaa tttttctgtc tggcgttttt 540

gtaatc 546

<210> 11
<211> 496
<212> DNA
<213> Homo Sapiens

<400> 11
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atatttggtg accttaagtg tacagaacac tgattcccca tcctatccag agattagttt 180

tagttgcagc atggaacaat tacaggactt ggtggggaaa cttaaagatg cttcgaaaag 240

cctggaaaga gcaactcagt tgtaacttgg ggaagttaac gatccgcccg agtgcagagg 300

aaaaccagaa acgccttgcc ttcagctgaa ccaccgtttg tgcgagctgg atgtcctttt 360

cagtagaaaa gaattttcct tttgaattta taccattcat caattttgac actttaaaaa 420

cgtgtgaaag ggttaagagg gaaagatact gcccaagtat ttgaatcgtt tagtagtaac 480

tgtccattta tcctat 496

<210> 12
<211> 313
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (190)..(190)
<223> n is a, c, g, or t

<400> 12
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caataattac ttagtatcat ctaatatgtg gttcatattt aaatttgttg ttttgagatg 120

ggtcttacaa ttggtttatt caattgcatt ttttctaact cgtgtctcaa gtgttttaaa 180

aatctactgn acttataatg acttatataa tgtatttctc attttacctt tcttccaaaa 240

gaggaaataa tggcaaacca tataatattg tacattcact gtcaaaaagc aaaccccttgt 300

tttgataact tgt 313

<210> 13
<211> 395
<212> DNA
<213> Homo Sapiens

<400> 13
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cttttgttcc aatgtcaatg tgaacgtcca catgaaacct acacactgtc atgcttcatc 120

attccctctc atctcaggta gaaggttgac acagttgtag ggttacagag acctatgtaa 180

gaattcagaa gacccctgac tcatcatttg tggcagtccc ttataattgg tgcatagcag 240

atggtttcca catttagatc ctggtttcat aacttcctgt acttgaagtc taaaagcaga 300

aaataaagga agcaagtttt cttccatgat tttaaattgt gatcgagttt taaattgata 360

ggagggaaca tgtcctaatt cttctgtcct gagaa 395

<210> 14
<211> 569
<212> DNA
<213> Homo Sapiens

<400> 14
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gttctgaagt tttacagatg gaacctgaca atgtgaatgc cctgaaagat cgagctgagg 120

cctatttgat agaggaaatg tatgatgaag ctattcagga ttatgaaact gctcaggaac 180

acaatgaaaa tgatcagcag attcgagaag gtctagagaa agcacaaaga ttattgaaac 240

agtcgcagaa acgagattat tataaaatct tgggagtaaa aagaaatgcc aaaaagcaag 300

aaattattaa agcataccga aaattagcac tgcagtggca cccagataac ttccagaatg 360

aagaagaaaa gaaaaaagct gagaaaaagt tcattgatat agcagctgct aaagaagtcc 420

tctctgatcc agaaatgaga aagaagtttg acgacggaga agatcctttg gatgcagaga 480

gccagcaagg aggcggcggc aacccctttcc acagaagctg gaactcatgg caagggttca 540

atcccttcag ctcaggcgga ccatttaga 569

<210> 15
<211> 481
<212> DNA
<213> Homo Sapiens

<400> 15
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gtagtagagc tatttcttgt acttctaagt tttctagaag tggaaggatt gtagtcatcc 120

tgaaaatggg tttacttcaa aatccctcag ccttgttctt cacgactgtc tatactgaga 180

gtgtcatgtt tccacaaagg gctgacacct gagcctggat tttcactcat ccctgagaag 240

ccctttccag tagggtgggc aattcccaac ttccttgcca caagcttccc aggctttctc 300

ccctggaaaa ctccagcttg agtcccagat acactcatgg gctgccctgg gcagccagca 360

ttcattgtaa gttccctctt tgaaaactgg tgtgtgggtg ttcagttctg tgtctggtgg 420

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<210> 16
<211> 398
<212> DNA
<213> Homo Sapiens

<400> 16
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gagcaggcga ccgagctcct tccccatcat ttctccttgg ccaacgacga ggccagccag 120

aatggcaata aggactccga atacataata aaagcaaaca gaacactcca acttagagca 180

ataacggctg ccgcagcagc cagggaagac cttggtttgg tttatgtgtc agtttcactt 240

ttccgataga aatttcttac ctcatttttt taagcagtaa ggcttgaagt gatgaaaccc 300

acagatccta gcaaatgtgc ccaaccagct ttactaaagg gggaggaagg gagggcaaag 360

ggatgagaag acaagtttcc cagaagtgcc tggttctg 398

<210> 17
<211> 499
<212> DNA
<213> Homo Sapiens

<400> 17
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aaggagaagc tgccgggaga gctagagccg gtgcaggcca cgcagaacaa gacagggaag 120

tatgtgccgc cgagcctgcg cgacggggcc agccgccgcg gggagtccat gcagcccaac 180

cgcagagccg acgacaacgc caccatccgt gtcaccaact tgtcagagga cacgcgtgag 240

accgacctgc aggagctctt ccggcctttc ggctccatct cccgcatcta cctggctaag 300

gacaagacca ctggccaatc caagggcttt gccttcatca gcttccaccg ccgcgaggat 360

gctgcgcgtg ccattgccgg ggtgtccggc tttggctacg accacctcat cctcaacgtc 420

gagtgggcca agccgtccac caactaagcc agctgccact gtgtactcgg tccgggaccc 480

ttggcgacag aagacagcc 499

<210> 18
<211> 261
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (41)..(42)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (196)..(196)
<223> n is a, c, g, or t

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gtttggggag agacacaggc aggcgagggg gctggtcccc agtctgttgg ggtggtgctc 180

agggtaaagg gctatnggca acaggggacc agaccaggga tgagtgggga gggcacaagg 240

accatttgcc agaatccacc g 261

<210> 19
<211> 526
<212> DNA
<213> Homo Sapiens

<400> 19
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tgcctttcac cacatggcct tgcctcggtg gccctgactg tcagggaggg ccagggaggc 120

agagcgggag ggagtctcag gaggaggctt gccctgaggg gctggggagg gggtacctca 180

tgaggaccag ggtggagctt gagaagagga ggaggtgggg gcttggaggt gcttggtagc 240

tgaggggacg ggcaagtgag aggggaggga gggaagtcct gggaggatcc tgagctgctg 300

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agaatggggg ctttcgggga gggcgcctag tccccccagc tctaagcagc caggagggac 420

ctgcatctaa gcatctgggt tgccatggca atggcatgcc ccccagctac tgtatgcccc 480

cgacccccgc agaggcagaa tgaacccata gggagctgat cgtaat 526

<210> 20
<211> 516
<212> DNA
<213> Homo Sapiens

<400> 20
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ccatcatccc cgagctggag cgtgagatcc gcatcatcaa cacggagcag tacatgcact 120

cgctgacgtg gcagcaggcg ctcacggggc tgctggagcg catgcagacc tatcaggacg 180

cggagtcgag gcaggtgctg gctgcctgga tgaaagagcg gcaggagctg aggtgcatca 240

ccaaggccct gttcaatgcg cagttcggca gcatcttccg caccttccac aaccccacct 300

acttctcaag gcgcctcgtg cgcttctctg acctctacat ggcctccctc agctgcctgc 360

tcaactaccg cgtggacttc accttctacc cacgccgtac gccgctgcag cacgaggcac 420

ccctctggat ggaccagctc tgcaccggct gcatgaagac cccttcctt ggtgacatgg 480

cccacatccg ctgagggcac ctttattgtc tgggac 516

<210> 21
<211> 482
<212> DNA
<213> Homo Sapiens

<400> 21
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cagtctaaat tctttcactt acatctttac agaaaactat attttctctc ttccataccc 120

agaaatctaa tcagaaaact gacttttctc atgttcaact ggacctaggg gaatatgaca 180

gaaaagcatc ccataggctt taatatactt tttaaaatat ataaaactga aaattaatag 240

ccatttaccc tgaaagagtt ctgcgtggac tttgtcactt gcatagtaat agcatgtgcc 300

tcattgttca gaagattagc tttaggtcct attttcaaat acgaaatggt agcataagct 360

gtaaaactgt agtcttctct gcagaaaata aaggccaaca ataagaaagc ttttgaagga 420

atcacggaaa acaaatttat aaaagaaata actatatgcg cagtaattct taacacattg 480

ac 482

<210> 22
<211> 459
<212> DNA
<213> Homo Sapiens

<400> 22
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acttcggcag cggagccatg ttgcatgatg tggtcctggg tgtgcccgaa aacgctctgc 120

agcccactca cccagtgtac aacattggac cagacaaggt gatccaggcc actacatact 180

ttctacagaa gccagtccca ggttttgagg agcttaagga tgagacatcg gcagagcctg 240

caaccgacta gaggacctgg gtcccggcag ctctttgctc acccatctcc ccagtcagac 300

aaggtttata cgtttcaata catactgcat tctgtgctac acaagcctta gcctcagtgg 360

agctgtggtt ctcttggtac tttcttgtca aacaaaacca atggctctgg gtttggagaa 420

cacagtggct ggttttaaaa ttctttccac acctgtcaa 459

<210> 23
<211> 549
<212> DNA
<213> Homo Sapiens

<400> 23
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cctcacaagc agtgacacct cgggtccttt ccgttgctat ggtgaaaatt cctggatgga 120

atggatcaca tgagggtttc ttgttgcttt tggagggtgt gggggatatt ttgttttggt 180

ttttctgcag gttccatgaa aacagccctt ttccaagccc attgtttctg tcatggtttc 240

catctgtcct gagcaagtca ttcctttgtt atttagcatt tcgaacatct cggccattca 300

aagcccccat gttctctgca ctgtttggcc agcataacct ctagcatcga ttcaaagcag 360

agttttaacc tgacggcatg gaatgtataa atgagggtgg gtccttctgc agatactcta 420

atcactacat tgctttttct ataaaactac ccataagcct ttaaccttta aagaaaaatg 480

aaaaaggtta gtgtttgggg gccgggggag gactgaccgc ttcataagcc agtacgtctg 540

agctgagta 549

<210> 24
<211> 372
<212> DNA
<213> Homo Sapiens

<400> 24
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cacctactct tatttactgc ccattgattg acttttcttc atattttgca aagagaaatt 120

tcacagcaaa aattcatgtt ttgtcagctt tctcatgttg agatctgtta tgtcactgat 180

gaatttaccc tcaagtttcc ttcctctgta ccactctgct tccttggaca atatcagtaa 240

tagctttgta agtgatgtgg acgtaattgc ctacagtaat gaaaaattaa tgtactttaa 300

tttttcattt tcttttagga tatttagacc acccttgttc cacgcaaacc agagtgtgtc 360

agtgtttgtg tg 372

<210> 25
<211> 475
<212> DNA
<213> Homo Sapiens

<400> 25
cagggatcgg aggacgaccc gagtcccaag agtggggttt tgctttttaa aaggagagag 60

gaggggtgat ggcaggggag tggagggtgg ccgggcaggt cctgccggcg cagggagccc 120

tctgcccttc acactctcct ccaaaagagc ctccatctgt aaggaagcag gtctccgcga 180

ggggtttctt tccatgtgtt ttcctcctgt tgttaaaaga actttttttaa aaaaacagac 240

ctcgttttag atttatagca ttgactttta cacacattca cacaagaaaa aaatcctttc 300

aaaattctta aatcttctgt tcctcctttt tccaagggaa gagggcaaaa agtggcctgg 360

gctctgttgg tgtgcgtgtt ccgtggcgga gagaagaaaa tgggaaagac atctcactgg 420

tgcttttctc ttttgtttta gtgccccccg cccccatccc tataatatct gtaac 475

<210> 26
<211> 516
<212> DNA
<213> Homo Sapiens

<400> 26
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ttacactttt atttcctgta tgttgtacaa tcaaaacaca ctactacctc ttaagtccca 120

gtatacctca tttttcatac tgaaaaaaaa agcttgtggc caatggaaca gtaagaacat 180

cataaaattt ttatatatat agtttatttt tgtgggagat aaattttata ggactgttct 240

ttgctgttgt tggtcgcagc taaataagac tggacattta acttttctac catttctgca 300

agttaggtat gtttgccagg agaaaagtat caagacgttt aactgcagtt gactttctcc 360

ctgttccttt gagtgtcttc taactttatt ctttgttctt tatgtagaat tgctgtctat 420

gattgtactt tgaatcgctt gacttgttga aaatatttct ctagtgtatt atcactgtct 480

gttctgcaca ataaacataa cagcctctgt gatccc 516

<210> 27
<211> 566
<212> DNA
<213> Homo Sapiens

<400> 27
gcgtttccaa cctcggagaa ttccaggcac tccccttccc cctccgctga catacttgta 60

taagcggtca tcgttgcgtc atggggcagg cgtggggagc ttcctgtcgc cttggctggg 120

tgtgggcctg gaggaaggtc ctggggcgtg cactcgcctg ggcagtgggg aggagagtgg 180

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cctgagttac ttcacccccg cgtgctgctg gttaatgtcc cgcgtctctg caccttcggg    240

tgggagcggg gactgatcta ctttcacatt ctcaagtttt tctcatctgc attagaggtc    300

cccagtaggt tcccaggttc cagcgtgccc ctccctcaga cacacggaca caatcagccg    360

agaagttcct ggtctgaatc acgagaatgt ggaggggtgg ggggtgtcag tggaaaggca    420

taaggctgag ctgagaccag ttgctggtga aactgggcca atctggggag gggaacatcc    480

ttgccaggga gtttctgagg gtctgctttg tttacctttc gtgcggtgga ttctttttaa    540

ctccgtctac ctggcgtttt gttaga                                         566


<210>  28
<211>  327
<212>  DNA
<213>  Homo Sapiens


<220>
<221>  misc_feature
<222>  (199)..(199)
<223>  n is a, c, g, or t

<400>  28
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agcccgagcc ggcacccaac tccgtgtcca tcacgggctc cgtggacgac cactttgcca    120

aagctctggg tgacacgtgg ctccagatca aagcggccaa ggacggagca tccagcagcc    180

ctgagtccgc ctctcgcang ggccagcccg ccagcccctc tgcccacatg gtcagccaca    240

gtcactcccc ctctgtggtc tcctgaaggg agcgcctcct ccaacaacac gtggatctgc    300

atggtttgcc tgagctttga acagtca                                        327


<210>  29
<211>  347
<212>  DNA
<213>  Homo Sapiens


<220>
<221>  misc_feature
<222>  (156)..(156)
<223>  n is a, c, g, or t

<400>  29
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tttttacttc cttctgggtg gaggctttcc gactcccaat catgaaggca agttaatctt    120

tccagttagt gacttttgcc ccatagttgg ggtaancact tcctagattg agaaaaagca    180

gctacagtca atcctgctct gtttgcctca tttggtgatc agtcagtcac acataagttc    240

cttgtattct aaatttcatg cacttctccc agatgctata gggtttctc tcactgttgc     300

caatggatgt catccagaca gtgggctcat atcttacggt tttgtgc                  347


<210>  30
<211>  210
<212>  DNA
<213>  Homo Sapiens

<400>  30
agttgatcag agccttccag agtgtggtat gcttttcact gtgtgatgat ccttagtggc     60
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acatgaatga acgtccagat gtttgtgcag tagcccaccc ttatctgcag gatacgttcc 120

aagacccccca gtgaatgcct gaaactgcag atagtactga atcctatata tactgtgttt 180

tttatgatac atacatgcct atgatgaagt 210

<210> 31
<211> 511
<212> DNA
<213> Homo Sapiens

<400> 31
aagagaatgt tcctactcac acttcagctg ggtcacatcc atccctccat tcatccttcc 60

atccatcttt ccatccatta cctccatcca tccttccaac atatatttat tgagtaccta 120

ctgtgtgcca ggggctggtg ggacagtggt gacatagtct ctgccctcat agagttgatt 180

gtctagtgag gaagacaagc atttttaaaa aataaattta aacttacaaa ctttgtttgt 240

cacaagtggt gtttattgca ataaccgctt ggtttgcaac ctctttgctc aacagaacat 300

atgttgcaag accctcccat gggggcactt gagttttggc aaggctgaca gagctctggg 360

ttgtgcacat ttctttgcat tccagctgtc actctgtgcc tttctacaac tgattgcaac 420

agactgttga gttatgataa caccagtggg aattgctgga ggaaccagag gcacttccac 480

cttggctggg aagactatgg tgctgccttg c 511

<210> 32
<211> 505
<212> DNA
<213> Homo Sapiens

<400> 32
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ttcagctgcc agtgtgttac tcatctttat cctaaaaatc tggaatcaga gatttttgtt 180

tgttcacata tgattctctt agacactttt atatttgaaa aaattaaaat ctttctttgg 240

ggaaaaattc ttggttattc tgccataaca gattatgtat taacttgtag attcagtggt 300

tcaatacctg tttagttgct tgctaatatt tccagaagga tttcttgtat tggtgaaaga 360

cggttgggga tggggggatt tttttgttct tgttgtaccc ttgttttgaa actagaaatc 420

tgtcctgtgg catgcaaaag aaagcaaatt atttttaaaa gaaaaaaacc aaagtacttt 480

tggtgtcatt attccatctt ctcca 505

<210> 33
<211> 307
<212> DNA
<213> Homo Sapiens

<400> 33
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acttgggtat ttaaaccatg tcagagctgc ctcaccacag gaccttgctg gaggctatac 120

ttcttctctt gcttgtcaca gagcactaca ggatgcattc agtgggcttt tctggcagcc 180

cagttaacca tttataagat ttggaccttg gagctgaacc agggagctag caaaagtaaa 240

gcagacttat aaaattatag ctatgtgcag ctgcacaaca cagtccttcc actagcagct 300

gtgttaa 307

<210> 34
<211> 519
<212> DNA
<213> Homo Sapiens

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<223> n is a, c, g, or t

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<222> (167)..(167)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (169)..(169)
<223> n is a, c, g, or t

<220>
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<222> (268)..(268)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (349)..(349)
<223> n is a, c, g, or t

<220>
<221> misc_feature
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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ggaacgcggg cggtgcggac tcagcgggcc gggtgcaggc gcggagctgg gcctctgcgc 120

ccggcccgan ctccgtctat aaanagagca gccagttgca gggctcnant ctgctttcca 180

actgcctgac tgcttgttcg tctcactggt gtgagctcca gcatcccctt tgctcgaaat 240

ggaccccaac tgctcttgcg ccactggntg gctcctgcac gtgcgccggc tcctgcaagt 300

gcaaagagtg caaatgcacc tcctgcaaga agagctgctg ttcctgctnc cccgtggnct 360

gtgccaagtg tgcccagggc tgcgtctgca aaggggcatc ggagaagtgc agctgctgtg 420

cctgatgtgg gaacagctct tctcccagat gtaaatagaa caacctgcac aacctggnat 480

ttttttaaaa atacaacact gagccatttg ctgcatttc 519

<210> 35

<211> 460
<212> DNA
<213> Homo Sapiens

<400> 35
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acctcccacc ctgcaaaggg aatctcttgc ctgctccatc tcataggcta agtcagctga 180

atcccgatag tactaggtcc ccttccctcc gcatcccgtc agctggaaaa ggcctgtggc 240

ccagaggctt ctccaaaggg agggtgacat gctggctttt gtgcccaagc tcaccagccc 300

tgcgccacct cactgcagta gtgcaccatc tcactgcagt agcacgccct cctgggccgt 360

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acgctgtggc cctgcctggc tagtccctgc ctgaataaag 460

<210> 36
<211> 540
<212> DNA
<213> Homo Sapiens

<400> 36
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atgctggtgg tgattttta gcccctaaat aaaacactgg actatttcct gtttacttca 120

ttgattgcaa ctacaaaggt ggactcaaag caaagcacaa tcatgccagc caacattcca 180

gaattctgct gagaactcca agtctgtgag gggagaggtt ttacaagcca gacaggcctg 240

ggggactgca gtccccaagg agaccctgcc acatgctggc cctttgagtg agaatgctgc 300

atctttctac atatcttcat gagaatactg agaattggat tttccttttc aaaatgcact 360

ttgctttttt tgtatgtttt gttatgttga gatgtttcta aagaaaagat tttatgtaat 420

tataagatga agcgtagtga attgtacagc tgttgtaata atgacctatt tctatataaa 480

ataaaattgt atggcttatg tgtaaattat tttgtatctg agataccagt tccttttccc 540

<210> 37
<211> 367
<212> DNA
<213> Homo Sapiens

<400> 37
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gtttgcaatg ctggtagaga tcacagagcg agccatggca cattgtggct cccaggaggc 180

cctcattgtg ggaggagtgg ggtgtaatgt gaggctacag gagatgatgg caacaatgtg 240

ccaggaacgt ggagcccggc tttttgctac agatgagaga ttctgtattg acaatggagc 300

gatgatagcc caggctggct gggagatgtt tcgggctgga cacaggaccc cactcagtga 360

ttctggg 367

<210> 38
<211> 532
<212> DNA
<213> Homo Sapiens

<400> 38
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agtccttcac cttgccaggt gccgtttctc ttccgtgaag gccactgccc aggtccccag 120

tgcgcccct agtggccata gcctggttaa agttccccag tgcctccttg tgcatagacc 180

ttcttctccc accccttct gcccctgggt ccccggccat ccagcggggc tgccagagaa 240

ccccagacct gcccttacag tagtgtagcg cccctccct ctttcggctg gtgtagaata 300

gccagtagtg tagtgcggtg tgcttttacg tgatggcggg tgggcagcgg gcggcgggct 360

ccgcgcagcc gtctgtcctt gatctgcccg cggcggcccg tgttgtgttt tgtgctgtgt 420

ccacgcgcta aggcgacccc ctccccgta ctgacttctc ctataagcgc ttctcttcgc 480

atagtcacgt agctcccacc ccaccctctt cctgtgtctc acgcaagttt ta 532

<210> 39
<211> 551
<212> DNA
<213> Homo Sapiens

<400> 39
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atagcctggt taaagttccc cagtgcctcc ttgtgcatag accttcttct cccacccct 180

tctgcccctg ggtccccggc catccagcgg ggctgccaga gaaccccaga cctgccctta 240

cagtagtgta gcgcccctc cctctttcgg ctggtgtaga atagccagta gtgtagtgcg 300

gtgtgctttt acgtgatggc gggtgggcag cgggcggcgg gctccgcgca gccgtctgtc 360

cttgatctgc ccgcggcggc ccgtgttgtg ttttgtgctg tgtccacgcg ctaaggcgac 420

cccctcccc gtactgactt ctcctataag cgcttctctt cgcatagtca cgtagctccc 480

accccaccct cttcctgtgt ctcacgcaag ttttatactc taatatttat atggcttttt 540

ttcttcgaca a 551

<210> 40
<211> 538
<212> DNA
<213> Homo Sapiens

<400> 40
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gctcgaagca ggtttaggac caggtcccct tgagaggtca gaggggcctc tgtgggtgct 120

gggtactcca gaggtgccac tggtggaagg gtcagcggag ccccagtgcc tccttgtgca 180

tagaccttct tctcccaccc ccttctgccc ctgggtcccc ggccatccag cggggctgcc 240

agagaacccc agacctgccc ttacagtagt gtagcgcccc ctccctcttt cggctggtgt 300

agaatagcca gtagtgtagt gcggtgtgct tttacgtgat ggcgggtggg cagcgggcgg 360

cgggctccgc gcagccgtct gtccttgatc tgcccgcggc ggcccgtgtt gtgttttgtg 420

ctgtgtccac gcgctaaggc gaccccctcc cccgtactga cttctcctat aagcgcttct 480

cttcgcatag tcacgtagct cccaccccac cctcttcctg tgtctcacgc aagtttta 538

<210> 41
<211> 403
<212> DNA
<213> Homo Sapiens

<400> 41
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ccatccggaa cagggccttc tacatggagg agggcgtgcc ctattgcgag cgagactatg 120

agaagatgtt tggcacgaaa tgccatggct gtgacttcaa gatcgacgct ggggaccgct 180

tcctggaggc cctgggcttc agctggcatg acacctgctt cgtctgtgcg atatgtcaga 240

tcaacctgga aggaaagacc ttctactcca agaaggacag gcctctctgc aagagccatg 300

ccttctctca tgtgtgagcc ccttctgccc acagctgccg cggtggcccc tagcctgagg 360

ggcctggagt cgtggccctg catttctggg tagggctggc aat 403

<210> 42
<211> 437
<212> DNA
<213> Homo Sapiens

<400> 42
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gcaggcctgt ggactttctc ctcgagacat taccactatt aaacttctca atgaaactag 120

agacatgttg gaaagcccag attttagtac agttttgaat acctgtttaa accgaggttt 180

tagtagactt ctagacaata tggctgagtt ctttcgacct actgaacagg acctgcaaca 240

tggtaactct atgaatagtc tttccagtgt cagcctgcct ttagctaaga taattccaat 300

agtaaacgga cagatccatt cagtttgcag tgaaacacct agtcattttg ttcaggatct 360

gttgacaatg gagcaagtga aagactttgc tgctaatgtg tatgaagctt ttagtacccc 420

tcagcaactg gagaaat 437

<210> 43
<211> 520
<212> DNA
<213> Homo Sapiens

<400> 43
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cggattccgg catccacatc atcctccgca ctgagtgagg gtggggagcc caggcctggc 120

ctcggggcag ggcagggcgg ctaggccggc cagctccccc ttgcccgcca gccagtggcc 180

gaacccccca ctccctgcca ccgtcacaca gtatttattg ttcccacaat ggctgggagg 240

gggcccttcc agattggggg ccctggggtc cccactccct gtccatcccc agttggggct 300

gcgaccgcca gattctccct taaggaattg acttcagcag ggtgggaggg ctcccagacc 360

cagggcagtg tggtgggagg ggtgttccaa agagaaggcc tggtcagcag agccgccccg 420

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cctctgttca gtcgcaaagg tgaacactca tgcggcagcc 520

<210> 44
<211> 530

<212> DNA
<213> Homo Sapiens

<220>
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<222> (68)..(68)
<223> n is a, c, g, or t

<400> 44
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tactagaata ttcaaaatca atcatgaagg cagttactat tttgagtcta aaggttttct 180

aaaaattaac ctcacatccc ttctgttagg gtctttcaga atatctttta taaacagaag 240

catttgaagt cattgctttt gctacatgat ttgtgtgtgt gaaggacata ccacgtttaa 300

atcattaatt gaaaaacatc atataagccc caactttgtt tggaggaaga gacggaggtt 360

gaggtttttc cttctgtata agcacctact gacaaaatgt agaggccatt caaccgtcaa 420

acaccatttg gttatatcgc agaggagacg gatgtgtaaa ttactgcatt gctttttttt 480

tcagtttgta taacctctaa tctccgtttg catgatacgc tttgttagaa 530

<210> 45
<211> 485
<212> DNA
<213> Homo Sapiens

<400> 45
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ggtctggttg atcgatgtca gtcagtcagt agaacctacc caccctcacg gcctggagtt 120

cttgttccgg gactgcagga atgtctcgca gtttttccag aaaggaggag tcaaggaagc 180

ccttagtgaa cgagaactct tcaatgctgt ttcaggctta aacatcacag cagataatga 240

agctgatttt ttagctgaga tagaagcttt ggagaaaatg aatgaagatc acgttcagaa 300

gaatggaagg aaagctgctt catttttgaa agatgatgga gacccaccac tactatatga 360

tgaatagcac taatacccac tgcttcagtg ttaacacagc agtgattgtc agctgccaat 420

agcaaatgaa gttatgggtg acttgaaata ccaaaacctg aggagtgggc aatggtgctt 480

ctgtg 485

<210> 46
<211> 351
<212> DNA
<213> Homo Sapiens

<400> 46
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cctcccaaag tgctaggatt acaggcataa gccactgagc ccagccctag ttcagtatct 120

tttatgtaaa ttataaacat ctgcaacatt atgtatcata tgcagatact tattgcattt 180

cttttattag tggtgaaagt gttctatgca tttattggct cttgaatttc ctcatctatg 240

aattgtcatt cacacaccta cttttctgct tcgtttttac atatgtcttt gcctattaaa 300

gatattatcc ctctgtttta tattttctct cattcttgta ttgcctttta a 351

<210> 47
<211> 521
<212> DNA
<213> Homo Sapiens

<400> 47
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ctcctcctcc aacaagcaga accaactctc tcctctggaa gggggcaagc cgctcatgtc 120

cagctcagaa gaggaattct cacctcccca aagtccagac cagaactcgg tccttctgct 180

gcagggcaat atgggccacg ccaggagctc aaactattct ctcccgggct taacagcctc 240

gcagcccagt cacggcctgc agacccacca gcatcagctc caagactctc tgctcggccc 300

cctcacctcc agtctggtgg acttggggtc ctaagtgggg agggactggg gcctcgaagg 360

gattcctgga gcagcaacca ctgcagcgac tagggacact tgtaaataga aatcaggaac 420

atttttgcag cttgtttctg gagttgtttg cgcataaagg aatggtggac tttcacaaat 480

atctttttaa aaatcaaaac caacagcgat ctcaagctta a 521

<210> 48
<211> 498
<212> DNA
<213> Homo Sapiens

<400> 48
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ctgtgcccgc aaaccagaca cataggacaa agtttatcta taacctggaa gaccatgagt 120

ggtgtgaaaa catggagtcc gttttatagt gactaaagga gggctgaact ctgtattagt 180

aatccaaggg tcattttttt cttaaaaaaa gaaaaaaagg ttccaaaaaa aaccaaaact 240

cagtacacac acacaggcac agatgcacac acacgcagac agacacaccg actttgtcct 300

ttttctcagc atcagagcca gacaggattc agaataagga gagaatgaca tcgtgcggca 360

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ccagcttgga ggatggac 498

<210> 49
<211> 331
<212> DNA
<213> Homo Sapiens

<400> 49
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aaggtaacag gcatctttct tctcagtgcc ttggccctgt tgagtctatc tggtaacact 120

ggagctgact ccctgggaag agaggccaaa tgttacaatg aacttaatgg atgcaccaag 180

atatatgacc ctgtctgtgg gactgatgga aatacttatc ccaatgaatg cgtgttatgt 240

tttgaaggtc ggaaacgcca gacttctatc ctcattcaaa aatctgggcc ttgctgagaa 300

ccaaggtttt gaaatcccat caggtcaccg c 331

<210> 50
<211> 548

<212> DNA
<213> Homo Sapiens

<400> 50
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attctgagat gtgcaaagac taccgagtat tgcccaggat aggctatctt tgtccaaagg 120

atttaaagcc tgtctgtggt gacgatggcc aaacctacaa caatccttgc atgctctgtc 180

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tgggaatgga atcactgatt ttcagtcttt tccatttctt tcctcctaga atctgtgatc 480

tgagggtata aagacatttc caccaagttt gagccctcaa aatgtcctga ttacaatgct 540

gtctgtcc 548

<210> 51
<211> 526
<212> DNA
<213> Homo Sapiens

<400> 51
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gtcattaaaa atacaccctc tacttgggct ttatactgca tacaaattta ctcatgagcc 120

ttcctttgag gaaggatgtg gatctccaaa taaagattta gtgtttattt tgagctctgc 180

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aggcttcacg gaaatagcat ggaaaaacaa tgcttccagt ggccacttcc taaggaggaa 420

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<210> 52
<211> 476
<212> DNA
<213> Homo Sapiens

<400> 52
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tgtacagagt acattggatc atgttggaaa gaaggcaagt gaaaaggtca gagatgaagt 120

agcgaagtta tggaatatcg tggaaaggat actagttgtg aaatggaaag agacaagtta 180

tagtacccca aaagcaaaac aagcaggaga tgcaagagat gccccaaaag gacaaagcaa 240

caattttctg ttgccacctt tataccggaa gactctgttg tagaagaaaa gaaggctttg 300

gtgcacctta tgtgggagga ggagggggcag ggcatgctga tgctgagcgt acaggcagac 360

aagagcgtag cctgctgttg cctccatcac tatgaaatga cttattttac ctgaaggacc 420

catggtttat gttcctctaa ttcctttcac tctccctaag ccctctgaga gagatg 476

<210> 53
<211> 501
<212> DNA
<213> Homo Sapiens

<400> 53
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ataagaaccg tgtacggagt cgtatctcca acctgaagga tgccaagaac cctgacctgc 120

ggcggaatgt gctgtgtggg gccataacac cccagcagat cgctgtgatg acctcagagg 180

agatggccag tgatgagctg aaggagatcc gtaaggccat gaccaaggag gccatccgag 240

agcaccagat ggcccgcact ggcggcacgc agacagacct gttcacctgc ggcaagtgca 300

ggaaaaagaa ctgcacctac acacaggtgc agacccgcag ctctgatgag cccatgacca 360

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tgtgctgcag ccttgggccc tccccggccc acgtcctccg ttgacacagc ttctctggag 480

accctagaag gcggcatgtc c 501

<210> 54
<211> 453
<212> DNA
<213> Homo Sapiens

<400> 54
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aggcagcctt cgacatcttc gtgctgggcg ctgaggatgg ctgcatcagc accaaggagc 120

tgggcaaggt gatgaggatg ctgggccaga accccacccc tgaggagctg caggagatga 180

tcgatgaggt ggacgaggac ggcagcggca cggtggactt tgatgagttc ctggtcatga 240

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gcatgtttga caaaaatgct gatggctaca tcgacctgga tgagctgaag ataatgctgc 360

aggctacagg cgagaccatc acggaggacg acatcgagga gctcatgaag gacggagaca 420

agaacaacga cggccgcatc gactatgatg agt 453

<210> 55
<211> 498
<212> DNA
<213> Homo Sapiens

<220>
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<222> (142)..(142)
<223> n is a, c, g, or t

<400> 55
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tgcctggcct gggctagggg cactgtctga actcctgact gtcaggataa actccgtggg 300

ggtacaggag cccagacaaa gcccaggcct gtcaagagac gcagagggcc cctgccaggg 360

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cacgtgctgg ccatgtggcc agggacggca tgagcaggag gcggggacgt gggggccttc     480

tggtttggtg tcaacagc                                                   498


<210>  56
<211>  544
<212>  DNA
<213>  Homo Sapiens

<400>  56
gaagccacaa agatgccaca tgttagtata tcagtgagag gtgactccac agtgctctct      60

ggagaagcaa tatgagtgac tgaagagtgg ggccttttgc ttttgcctgg atataggggt     120

gctcttctac tgtaattggg tgtggaaaaa ctctggcttt atggtattcc attaggttct     180

tttcatttaa agtagtctta aaatcaaagt atccaatatt ttaaagccac aaagtagatt     240

acataattag cagagatttt agtcagtaaa atgttagaaa tcaaactata agaaaattca     300

agtcctttat tttgtgtctt gggtatatgt cattatttta aattccacac tcccttattt     360

aatcactttg gtaagtgcct ttgatgtttt gaaatgtata gtgggagatg agcaaatgta     420

aatgtcatgt gccctgttcc ctagcttctc aattcctcat aaccattttt accagtgttg     480

caaagtttag acctttgtgt taatatcaga agtgtatttg tagcccctcc atagtgaaca     540

atga                                                                  544


<210>  57
<211>  535
<212>  DNA
<213>  Homo Sapiens

<400>  57
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cttcctgtcc aagatccggt cccacgtggc tacttgttcc aaataccaga attacatcat     180

ggaaggtgtg aaggccacca ttaaggatgc atctcttcag ccaaggaatg tcccaaaccg     240

ttacaccttt ccttgtcctt actgtcctga gaagaacttt gatcaggaag gacttgtgga     300

acactgcaaa ttattccata gcacggatac caaatctgtg gtttgtccga tatgtgcctc     360

gatgccctgg ggagacccca actaccgcag cgccaacttc agagagcaca tccagcgccg     420

gcaccggttt tcttatgaca cttttgtgga ttatgatgtt gatgaagagg acatgatgaa     480

tcaggtgttg cagcgctcca tcatcgacca gtgagcagag tccgtgcttg ctatc          535


<210>  58
<211>  479
<212>  DNA
<213>  Homo Sapiens

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cagcagaaag agaaatggaa tgtgcacgga tacacattca ctgctcagta agaggctcaa     120

gacatgactg atttgcattt taaagcaaga tgcgatgtcc agagttacag agaatgagta     180
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gatgtgtctc atcggttaat agctctatta tacctctaaa ggtggaattg tcagtttaga 240

ttcataaatg aaaaggtaaa tgagtaatca gaataaacca agtgataatc aaaccatgtc 300

aagattatta gttcagactc tagcctgtta attttcttag ttgatttctg aagctacctg 360

atttattcta ttaaattgta agcttgcaaa ctcaaaataa attggcagat ttacctctca 420

tgttttaatg tgtcaaatta gagagcaaag tataacaggt gccttcactt ttgagactt 479

<210> 59
<211> 518
<212> DNA
<213> Homo Sapiens

<400> 59
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ggtccatatt tagtggtact ctgaaattgg tcactttcct attacacgga gtgtgctaaa 180

actaaaaagc attttgaaac atacagaatg ttctattgtc attgggaaat tttctttctt 240

aacccagtgg aggttagaaa gaagttatat tctggtagca aattaacttt acatcctttt 300

tcctacttgt tatggttgtt tggaccgata agtgtgctta atcctgaggc aaagtagtga 360

atatgtttta tatgttatga agaaaagaat tgttgtaagt ttttgattct actcttatat 420

gctggactgc attcacacat ggcatgaaat aagtcaggtt ctttacaaat ggtattttga 480

tagatactgg attgtgtttg tgccatattt gtgccatt 518

<210> 60
<211> 489
<212> DNA
<213> Homo Sapiens

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aactttacaa atccatgaag ggtgctggca cagatgagaa gactctgacc aggatcatgg 120

tatcccgcag tgagattgac ctgctcaaca tccggaggga attcattgag aaatatgaca 180

agtctctcca ccaagccatt gagggtgaca cctccggaga cttcctgaag gccttgctgg 240

ctctctgtgg tggtgaggac tagggccaca gctttggcgg gcacttctgc caagaaatgg 300

ttatcagcac cagccgccat ggccaagcct gattgttcca gctccagaga ctaaggaagg 360

ggcaggggtg gggggagggg ttgggttggg ctcttatctt catggagctt aggaaacgct 420

cccactccca cgggccatcg agggccagca cggctgagcg gtgaaaaacc gtagccatag 480

atcctgtcc 489

<210> 61
<211> 472
<212> DNA
<213> Homo Sapiens

<400> 61
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atgcaaatgt cagcaagaat atttcggtga acggtgtggg gaaaagtcca tgaaaactca 120

cagcatgatt gacagtagtt tatcaaaaat tgcattagca gccatagctg cctttatgtc 180

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tgctgtgatc ctcacagctg ttgctgttat tacagtccag cttagaagac aatacgtcag    240

gaaatatgaa ggagaagctg aggaacgaaa gaaacttcga caagagaatg gaaatgtaca    300

tgctatagca taactgaaga taaaattaca ggatatcaca ttggagtcac tgccaagtca    360

tagccataaa tgatgagtcg gtcctctttc cagtggatca taagacaatg gaccctttt    420

gttatgatgg ttttaaactt tcaattgtca ctttttatgc tatttctgta ta            472
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<210>  62
<211>  523
<212>  DNA
<213>  Homo Sapiens


<220>
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<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (440)..(440)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (442)..(442)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (485)..(486)
<223>  n is a, c, g, or t

<220>
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<222>  (488)..(491)
<223>  n is a, c, g, or t

<220>
<221>  misc_feature
<222>  (493)..(498)
<223>  n is a, c, g, or t

<400>  62
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tgtttgccca gtttctgata tactgtacaa aggcgagaca atacacattc caactatgga    120

gaatggtcct aagctggcaa gccgcatctt gagcaaatta actgatatcc agtatggaag    180

agaagagagc gactggacaa ttgtgctatc ctgaatggaa aatagaggat acaatggaaa    240

atagaggata ccaactgtat gctactggga cagactgttg catttgaatt gtgatagatt    300

tctttggcta cctgtgcata atgtagtttg tagtatcaat gtgttacaag agtgattgtt    360

tcttcatgcc agagaaaatg aattgcaatc atcaaatggt gtttcataac ttggtagtag    420

taacttacct taccttaccn anaaaaatat taatgtaagc catataacat gggattttcc    480

tcaannannn nannnnnncc ttttgtactt cactcagata cta                      523
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<210>  63
<211>  373
<212>  DNA
<213>  Homo Sapiens
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<400> 63
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aactgtgaag atctgacttc gccccccccc ccccccatct tcgggaccag gatttgcaca 120

gaagcacatg cacctaccca tacacccccct cttctgagcg tccctgttcc cccatctcgc 180

tccctcccag gactctgacc ccagcattct caggcaccag tccctgtccg gaatgccacc 240

cacatcttcc atttccatgt cccctcccag agctggtgga cccagggaac agccactccc 300

ctccactctc taccagataa ctgaggaggg gagaggtggg ccgtaacggg cacggatcac 360

gatgtaaatt att 373

<210> 64
<211> 535
<212> DNA
<213> Homo Sapiens

<400> 64
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tgagaatcgc ggacaagaag tactacccca gctcccagga ctccagctcc gctgcggcgc 120

cccagctgct gattgtgctg ctgggcctca gcgctctgct gcagtgagat cccaggaagc 180

tggcacatct tggaaggtcc gtcctgctcg gcttttcgct tgaacattcc cttgatctca 240

tcagttctga gcgggtcatg ggcaacacg gttagcgggg agagcacggg gtagccggag 300

aagggcctct ggagcaggtc tggaggggcc atggggcagt cctgggtgtg gggacacagt 360

cgggttgacc cagggctgtc tccctccaga gcctccctcc ggacaatgag tccccccctct 420

tgtctcccac cctgagattg ggcatggggt gcggtgtggg gggcatgtgc tgcctgttgt 480

tatgggtttt ttttgcgggg ggggttgctt ttttctgggg tctttgagct ccaaa 535

<210> 65
<211> 452
<212> DNA
<213> Homo Sapiens

<400> 65
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cgcccgcctc caggagctgc tggagtccaa ccggcagaca cgcctggagt tccagcagca 120

gctcggggag gcccccagtg atgccagccc ctaggctcca agagccccca accgggaccc 180

aaccctgcct ccctgggcta ggctctggcc tgggcactca ccccctggct tagacacctt 240

ctcaagggct ggccttcagg gacccctggt gggtctgcct gcctgggcca cccttcctgc 300

ctgggcctcc ccttggccta cctgggccag cccccaccac ctggcatgcc ctcctggggc 360

caagagtggg cctgcaaccc acccacttgc ctgcccaccc aactcctggg cgctccccac 420

tctgcccagg ccttgagtgt ccacattaaa tg 452

<210> 66
<211> 323
<212> DNA
<213> Homo Sapiens

<400> 66
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ggttgtaaat tagaaaagct gggattacat atggtgtgcg gttacagtct aaattttttc 120

atcctcctat gcatcataag catgtttgta atattttcaa aaatagttct actgatgcta 180

caggaatttc aagcctgtgg tgaatgttag tatttaccat agggagtgaa gtggagttat 240

ggtttcattc aatagagtat tgctgattat acttgagtgg aatcctttcc tcacgtactc 300

ccacagacgt ctgggcctgg aaa 323

<210> 67
<211> 560
<212> DNA
<213> Homo Sapiens

<400> 67
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cacagatgtg aagttcattt ccaatccgcc ctccatggtg gcagcgggga gcgtggtggc 120

cgcagtgcaa ggcctgaacc tgaggagccc caacaacttc ctgtcctact accgcctcac 180

acgcttcctc tccagagtga tcaagtgtga cccggactgc ctccgggcct gccaggagca 240

gatcgaagcc ctgctggagt caagcctgcg ccaggcccag cagaacatgg accccaaggc 300

cgccgaggag gaggaagagg aggaggagga ggtggacctg gcttgcacac ccaccgacgt 360

gcgggacgtg gacatctgag ggcgccaggc aggcgggcgc caccgccacc cgcagcgagg 420

gcggagccgg ccccaggtgc tcccctgaca gtccctcctc tccggagcat tttgatacca 480

gaagggaaag cttcattctc cttgttgttg gttgtttttt cctttgctct ttccccttc 540

catctctgac ttaagcaaaa 560

<210> 68
<211> 471
<212> DNA
<213> Homo Sapiens

<400> 68
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acaccataat gctaatttaa agagactcca aatctcaatg aagccagctc acagtgctgt 120

gtgccccggt catctagcaa gctgccgaac caaaagaatt tgcaccccgc tgcgggccca 180

cgtggttggg gccctgccct ggcagggtca tcctgtgctc ggaggccatc tcgggcacag 240

gcccaccccg ccccacccct ccagaacacg gctcacgctt acctcaacca tcctggctgc 300

ggcgtctgtc tgaaccacgc gggggccttg agggacgctt tgtctgtcgt gatggggcaa 360

gggcacaagt cctggatgtt gtgtgtatcg agaggccaaa ggctggtggc aagtgcacgg 420

ggcacagcgg agtctgtcct gtgacgcgca agtctgaggg tctgggcggc g 471

<210> 69
<211> 518
<212> DNA
<213> Homo Sapiens

<400> 69
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gctcttgctg tttcttcgga ggagagcggt ggtcaaagag cccttactgc ccccagagga 120

tgacacccgg gacaacgttt attactatga tgaagaagga ggcggagaag aggaccagga 180

ctttgacttg agccagctgc acaggggcct ggacgctcgg cctgaagtga ctcgtaacga 240

cgttgcacca accctcatga gtgtcccccg gtatcttccc cgccctgcca atcccgatga 300

aattggaaat tttattgatg aaaatctgaa agcggctgat actgacccca cagccccgcc 360

ttatgattct ctgctcgtgt ttgactatga aggaagcggt tccgaagctg ctagtctgag 420

ctccctgaac tcctcagagt cagacaaaga ccaggactat gactacttga acgaatgggg 480

caatccgttc aagaagctgg ctgacatgta cggaggcg 518

<210> 70
<211> 182
<212> DNA
<213> Homo Sapiens

<400> 70
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gggcatttct tgcgagcctc gcagcctccg gaagctgtcg acttcatgac aagcattttg 120

tgaactaggg aagctcaggg gggttactgg cttctcttga gtcacactgc tagcaaatgg 180

ca 182

<210> 71
<211> 538
<212> DNA
<213> Homo Sapiens

<400> 71
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agcgcccgag tggcggagct gctgctgctc cacggcgcgg agcccaactg cgccgacccc 120

gccactctca cctgacccgt gcacgacgct gcccgggagg gcttcctgga cacgctggtg 180

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gacctggctg aggagctggg ccatcgcgat gtcgcacggt acctgcgcgc ggctgcgggg 300

ggcaccagag gcagtaacca tgcccgcata gatgccacgg aaggtccctc agacatcccc 360

gattgaaaga accagagagg ctctgagaaa cctcgggaaa cttagatcat cagtcaccga 420

aggtcctaca gggccacaac tgcccccgcc acaacccacc ccgctttcgt agttttcatt 480

tagaaaatag agcttttaaa aatgtcctgc cttttaacgt agatatatgc cttccccc 538

<210> 72
<211> 513
<212> DNA
<213> Homo Sapiens

<400> 72
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tcgtcaaatg tcaaatattc tctctttggc tggaatgaca aaaactcaaa taaatgtatg 120

attaggagga catcataacc tatgaatgat ggaagtccaa aatgatggta actgacagta 180

gtgttaatgc cttatgttta gtcaaactct catttaggtg acagcctggt gactccagaa 240

tggagccagt catgctaaat gccatatact cacactgaaa catgaggaag caggtagatc 300

ccagaacaga caaaactttc ctaaaaacat gagagtccag gctgtctgag tcagcacagt 360

aagaaagtcc tttctgcttt aactcttaga aaaaagtaat atgaagtatt ctgaaattaa 420

ccaatcagtt tatttaaatc aatttattta tattcttctg ttcctggatt cccattttac 480

aaaacccact gttctactgt tgtattgccc agt 513

<210> 73
<211> 530
<212> DNA
<213> Homo Sapiens

<400> 73
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ttctatgtgg gatgattact tttttaagga ggattaattc tgaggtagta tagtaactaa 120

aggggaatat atgaattgtt taacaaatta gaatttgttt acaactactt gaatttttaa 180

attatgtcaa aacttacatt acttgccaag cagtatgatg ttataggaaa cataaataag 240

attacagagg tatcaatttg gttaaaattc accattttat aagactaagc aataatctta 300

acaacctctt tcctgaatat ttaaatgtgt ttgtatggtg ttatgactaa ttgttactga 360

tttagagact aagccctctt aaaaccttta gttaaatata aaaagaaatt atatatatct 420

tgcctccctg atggaaaact atataaaatt gtagacttaa aaggtttgtg gaaatacatt 480

aggatatcag aaaactaaat àtatggagtt gctttatgac tattacatgt 530

<210> 74
<211> 406
<212> DNA
<213> Homo Sapiens

<400> 74
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tccaccaaca acccctccca ggctaagctg cggcgggagc tcgacgaatc cctccaggtc 120

gctgagaggt tgaccaggaa atataacgag ctgctaaagt cctaccagtg gaagatgctc 180

aacacctcct ccttgctgga gcagctgaac gagcagttta actgggtgtc ccggctggca 240

aacctcacgc aaggcgaaga ccagtactat ctgcgggtca ccacggtggc ttcccacact 300

tctgactcgg acgttccttc cggtgtcact gaggtggtcg tgaagctctt tgactctgat 360

cccatcactg tgacggtccc tgtagaagtc tccaggaaga acccta 406

<210> 75
<211> 286
<212> DNA
<213> Homo Sapiens

<400> 75
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accagtacta tctgcgggtc accacggtgg cttcccacac ttctgactcg gacgttcctt 120

ccggtgtcac tgaggtggtc gtgaagctct ttgactctga tcccatcact gtgacggtcc 180

ctgtagaagt ctccaggaag aaccctaaat ttatggagac cgtggcggag aaagcgctgc 240

aggaataccg caaaaagcac cgggaggagt gagatgtgga tgttgc 286

<210> 76

<211> 436
<212> DNA
<213> Homo Sapiens

<400> 76
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tccgttttca ttgttcactt ctaaaccaaa aattatgtgt tgccaaaacc aaacccaggt 120

tcatgaatat ggtgtctatt atagtgaaac atgtactttg agcttattgt ttttattctg 180

tattaaatat tttcagggtt ttaaacacta atcacaaact gaatgacttg acttcaaaag 240

caacaacctt aaaggccgtc atttcattag tattcctcat tctgcatcct ggcttgaaaa 300

acagctctgt tgaatcacag tatcagtatt ttcacacgta agcacattcg ggccatttcc 360

gtggtttctc atgagctgtg ttcacagacc tcagcagggc atcgcatgga ccgcaggagg 420

gcagattcgg accact 436

<210> 77
<211> 429
<212> DNA
<213> Homo Sapiens

<400> 77
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cgtcccccgg ctcctgcctg gaggagttta gaagtgcgcc attcatcgag tgtcacggcc 120

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gcgagatgtt caagaagcct acgccgtcca ccttgaaggc aggggagctg cgcacgcacg 240

tcagccgctg ccaagtctgt atgagaagaa cataatgaag cctgactcag ctaatgtcac 300

aacatggtgc tacttcttct tctttttgtt aacagcaacg aaccctagaa atatatcctg 360

tgtacctcac tgtccaatat gaaaaccgta aagtgcctta taggaatttg cgtaactaac 420

acaccctgc 429

<210> 78
<211> 195
<212> DNA
<213> Homo Sapiens

<400> 78
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gatccatcca tctccaggga gcaagacaga gacgcaggat ggaaagcgga gttcctaaca 120

ggatgaaagt tcccccatca gttcccccag tacctccaag caagtagctt tccacatttg 180

tcacagaaat cagag 195

<210> 79
<211> 301
<212> DNA
<213> Homo Sapiens

<400> 79
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gcaatgtcac aacctctctg atcttgtgct cagcatgatt ctttaataga agttttattt 120

ttcgtgcact ctgctaatca tgtgggtgag ccagtggaac agcgggagcc tgtgctggtt 180

tgcagattgc ctcctaatga cgcggctcaa aaggaaacca agtggtcagg agttgtttct 240

gacccactga tctctactac cacaaggaaa atagtttagg agaaaccagc ttttactgtt 300

t 301

<210> 80
<211> 459
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (164)..(164)
<223> n is a, c, g, or t

<400> 80
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tgtcaaaata agttttgttt tgttttgttt atgttgggtt tttaatgttg tctcttgacc 120

cttaatgctc aggttcttgt gggagttaat cagccacatc caangttacc ttgaggggga 180

agaagagggt gatgctcaga agctaaacaa gacaggggcc acatgaccct ctattgatta 240

gccccaagta gaaagtcctg tggttttatg tttaatggta atagttgatc atatatggca 300

taattttcta tcagcttcct actcagtcac tataaacaca gacttgaaat agtactttaa 360

atgtccaaat acctaaatgt gctaaactgg aggtaactat ttctaggtag ttgaattttt 420

gaaagtcatg atcagccaca caactgtttt gtacatact 459

<210> 81
<211> 394
<212> DNA
<213> Homo Sapiens

<400> 81
aatccttatt gttcagagtt gtttgggggt tctgtttcag agcataaaac ctaaaggtta 60

tagtagaaca aggcaccttc ttaaaagaaa tcttgcttca gaccatcagt tacagagaat 120

ttcctaaagt aaaattgaag caactacaac ttctccttag acactttgga atctaaccac 180

ttaaggacct ttttaaagag atagcttctc ttctttctga agatcaattt ctcccaaggc 240

caagattgtc cttttctccc atttcttgct agctattgca aatgagggaa gaacattatt 300

catctctcct ccccttttttt ttctgattct tttttcagtc agttttgctc ctgggttcaa 360

gtagtattac caccctttca caagcaacag actc 394

<210> 82
<211> 514
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (89)..(89)
<223> n is a, c, g, or t

<400> 82
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tgctcaaacc agatcgaagt ttgtctctna aagctattgt ctgcacaggc tgctgcatgc 120

tctgttgtta aatggatgga caggctattc taaattttgg ttgatacttt tgctactatg 180

ggcaattaac ttgaaaaaaa taatcgatcc caactctgtg ctctgatgta cctcttctgc 240

ccttttatg acacctttga ccaaatgcct tctatggttc acagtgcagg cacaaaacta 300

cctctgatac agaaggttct ttacaagctt attttacata ccgtgaatcc ctcacctaaa 360

gggagaggtg aaagcaaaga ctgctttgaa tgggtattga gggagattgt gtccatacca 420

agccaccctg aagaagtatt tcacttgcag tagaactgtg gatttgtgct gtcatttcac 480

cttggaataa acacctatct ctaagcagga ccaa 514

<210> 83
<211> 299
<212> DNA
<213> Homo Sapiens

<400> 83
caccaaatta cctaggctga ggttagagag attggccagc aaaaactgtg ggaagatgaa 60

ctttgtcatt atgatttcat tatcacatga ttatagaagg ctgtcttagt gcaaaaaaca 120

tacttacatt tcagacatat ccaaagggaa tactcacatt ttgttaagaa gttgaactat 180

gactggagta aaccatgtat tcccttatct tttactttt ttctgtgaca tttatgtctc 240

atgtaatttg cattactctg gtggattgtt ctagtactgt attgggcttc ttcgttaat 299

<210> 84
<211> 219
<212> DNA
<213> Homo Sapiens

<400> 84
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attagctttc tcctcatcca tttcttttat acctttcctt tttggggagt tgttatgcca 120

tgatttttgg tatttatgta aaaggattat tactaattct atttctctat gtttattcta 180

gttaaggaaa tgttgagggc aagccaccaa attacctag 219

<210> 85
<211> 518
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (61)..(65)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (71)..(71)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (73)..(73)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (112)..(112)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (163)..(163)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (295)..(295)
<223> n is a, c, g, or t

<400> 85
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nnnnncagca ncnatacaat aaggagggtt ttaatgtgaa gcaggcaatc tnccagcccc 120

ttctggtctt ggatgaaata gttgcacaga gtattgcacc aanaatacac aatggaggct 180

gaaaagttca acatatttta agtcaattaa tcaaattgca ttgattcttg atgctttctt 240

agaggcctac atgatttctt agattgctct gataaactat cataaggggt ccacntcccc 300

tcatttagct cccccaggga tttcttttcc cccatgtcat acacccagtc ctaaatcaac 360

ccccaaggct atccttccat cccttctgca gagggaactt ttgtcagact ctgcaacaaa 420

ctcctagctc tatccagagt gtcctctgct gctaagattg gtatctttct cctcaaaagc 480

ctggatggtg aatgggggtg cattagtcag aattctcc 518

<210> 86
<211> 458
<212> DNA
<213> Homo Sapiens

<400> 86
taaaaacctg tatctgaccc actttgtaat ttttgctcca atatccattc tgtagacttt 60

tgaaaaaaaa gtttttaatt tgatgcccaa tatattctga ccgttaaaaa attcttgttc 120

atatgggaga agggggagta atgacttgta caaacagtat ttctggtgta tattttaatg 180

tttttaaaaa gagtaatttc atttaaatat ctgttattca aatttgatga tgttaaatgt 240

aatataatgt attttctttt tattttgcac tctgtaattg cactttttaa gtttgaagag 300

ccattttggt aaacggtttt tattaaagat gctatggaac ataaagttgt attgcatgca 360

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tgtgttcaat atcagctttg ataattgtgt accttaag 458

<210> 87
<211> 336
<212> DNA
<213> Homo Sapiens

<400> 87
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tgctgtttct atgtcgtgga agcaccggat gggggtagtg agcaaatctg ccctgctcag 120

cagtcaccat agcagctgac tgaaaatcag cactgcctga gtagttttga tcagtttaac 180

ttgaatcact aactgactga aaattgaatg ggcaaataag tgcttttgtc tccagagtat 240

gcgggagacc cttccacctc aagatggata tttcttcccc aaggatttca agatgaattg 300

aaatttttaa tcaagatagt gtgctttatt ctgttg 336

<210> 88
<211> 521
<212> DNA
<213> Homo Sapiens

<400> 88
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ataaagtcag aaaataaagt taacataact ttcactaaca cacacatatg tagatttcac 120

aaaatccacc tataattggt caaagtggtt gagaatatat tttttagtaa ttgcatgcaa 180

aatttttcta gcttccatcc tttctccctc gtttcttctt tttttggggg agctggtaac 240

tgatgaaatc ttttcccacc ttttctcttc aggaaatata agtggttttg tttggttaac 300

gtgatacatt ctgtatgaat gaaacattgg agggaaacat ctactgaatt tctgtaattt 360

aaaatatttt gctgctagtt aactatgaac agatagaaga atcttacaga tgctgctata 420

aataagtaga aaatataaat ttcatcacta aaatatgcta ttttaaaatc tatttcctat 480

attgtatttc taatcagatg tattactctt attatttcta t 521

<210> 89
<211> 503
<212> DNA
<213> Homo Sapiens

<400> 89
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gagccaaaat tttccggcgt gaccaaggga aagtgactga tacggcatcc atgaaatata 120

tcatgcgata caacaattat aagaaggatc cttacagtag aggtgacccc tgtaatacca 180

tctgctgccg tgaggacctg aactcaccta acccaagtcc tggaggttgt tatgacacaa 240

aggtggcaga tatctaccta gcatctcagt acacatccta tgccataagt ggtcccacag 300

tacaaggtgg cctccctgtt tttcgctggg accgtttcaa caaaactcta catcagggca 360

tgccagaggt ctacaacttt gattttatta ccatgaaacc aattttgaaa cttgatataa 420

aatgaaggag ggagatgacg gactagaaga ctgtaaataa gataccaaag gcactatttt 480

agctatgttt ttcccatcag aat 503

<210> 90
<211> 275
<212> DNA
<213> Homo Sapiens

<400> 90
ccccatcacg gagggtccag actgtccact cgggggtgga gtgagactga ctgcaagccc 60

caccctcctt gagactggag ctgagcgtct gcatacgaga gacttggttg aaacttggtt 120

ggtccttgtc tgcaccctcg acaagaccac actttgggac ttgggagctg gggctgaagt 180

tgctctgtac ccatgaactc ccagtttgcg aattaataag agacaatcta ttttgttact 240

tgcacttgtt attcgaacca ctgagagcga gatgg 275

<210> 91
<211> 405
<212> DNA

<213> Homo Sapiens

<400> 91
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gtggaagttt atgctaatat tgtgtaactg atattaaacc taaatgttct gcctaccctg 120

ttggtataaa gatattttga gcagactgta aacaagaaaa aaaaaatcat gcattcttag 180

caaaattgcc tagtatgtta atttgctcaa aatacaatgt ttgattttat gcactttgtc 240

gctattaaca tccttttttt catgtagatt tcaataattg agtaatttta gaagcattat 300

tttaggaata tatagttgtc acagtaaata tcttgttttt tctatgtaca ttgtacaaat 360

ttttcattcc ttttgctctt tgtggttgga tctaacacta actgt 405

<210> 92
<211> 375
<212> DNA
<213> Homo Sapiens

<400> 92
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tttccctttg agtcatgatg acagatggtg tgaaaaccat ctaagtttgc ttttgaccat 120

cacctcccag tagcaatttg ctttcataat ccatttagca atccaggcct ctgttgaaaa 180

gataatatga gggagaaggg aacacatttc cttctgaact tacttcccta agtcactttc 240

cttatgtatc atctaataca atgatggttg agtgaaaata cagaaggggt gtttgagtat 300

tcagatttca taaaacactt ccttggaata tagctgcatt aacttggaaa gaagcctgtt 360

gggccagaag acaga 375

<210> 93
<211> 533
<212> DNA
<213> Homo Sapiens

<400> 93
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atgcaaagtt aagatcgaat ccatccgctt gtaggggaaa aaaaggaaaa aaattaacca 120

gagagggtct gtaatctcgc agagcacagg cagaatcgtt ccttccttgc tgcatttcct 180

ccttagacta atagacgttt tggaaagttc ggctagtgtt cgtgtgtttg tcgtagcacc 240

cagagcctcc accaaaccct ctccatgtct ttacctccca gtcgctctaa gatctgcttg 300

aagtctcgta tttgtactgc tttctgcttt tctcccaccc ctcctagcac ccccacatcc 360

cccatctagt aacatctcag aaatttcatc cagaggaaca aaaaaattaa aaatagaaca 420

tagcaaagca aagacagaat gccccccccc aaatattgtc ctgtccctgt ctgggagttg 480

tgttatttaa agatattctg tatgttgtat cttttgcatg tagcttcctt aat 533

<210> 94
<211> 413
<212> DNA
<213> Homo Sapiens

<400> 94
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aagctcaagt cccagtggaa caatgataat cccctttca agagcgccac cacgacggtc 120

atgaacccca agtttgctga gagttaggag cacttggtga agacaaggcc gtcaggaccc 180

accatgtctg ccccatcacg cggccgagac atggcttggc cacagctctt gaggatgtca 240

ccaattaacc agaaatccag ttattttccg ccctcaaaat gacagccatg gccggccggt 300

gcttctgggg gctcgtcggg gggacagctc cactctgact ggcacagtct ttgcatggag 360

acttgaggag ggcttgaggt tggtgaggtt aggtgcgtgt ttcctgtgca agt 413

<210> 95
<211> 465
<212> DNA
<213> Homo Sapiens

<400> 95
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ccacccgagg gccagtgagt cggggaagag gacttctcac tcccagagca agaggagtcc 120

ccccaactgg gtacagacct ccaccgccac ccccgacaca agagacttat ggagaatatg 180

actatgatga tggatatggc actgcttatg atgaacagag ttatgattcc tatgataaca 240

gctatagcac cccagcccaa agtggtgctg attactatga ttacggacat ggactcagtg 300

aggagactta tgattcctac gggcaagaag agtggactaa ctcaagacac aaggcacctt 360

cagcgaggac agcaaagggc gtctacagag accagccata tggcagatac tgattgtact 420

gtctgatgtt gtgaaatagc caatctccac cagtcctgta tactg 465

<210> 96
<211> 537
<212> DNA
<213> Homo Sapiens

<400> 96
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ctcatcagca gcatcgaggc ccagctgagc gagctccgca gtgagatgga gtgccagaac 120

caagagtaca agatgctgct ggacatcaag acacgtctgg agcaggagat cgccacctac 180

cgcagcctgc tcgagggcca ggacgccaag aagcgtcagc ccccgtagca cctctgttac 240

cacgacttct agtgcctctg ttaccaccac ctctaatgcc tctggtcgcc gcacttctga 300

tgtccgtagg ccttaaatct gcctggcgtc ccctccctct gtcttcagca cccagaggag 360

gagagagccg gcagttccct gcaggagaga ggaggggctg ctggacccaa ggctcagtcc 420

ctctgctctc aggacccccт gtcctgactc tctcctgatg gtgggccctc tgtgctcttc 480

tcttccggtc ggatctctct cctctctgac ctggatacgc tttggtttct caacttc 537

<210> 97
<211> 372
<212> DNA
<213> Homo Sapiens

<400> 97
aactttaact tagagcttca ttactttaag aatggaaaac aacctctgag tttgatttcc 60

caaagtttca taaagcccct aagctcatga ttttcatcaa ctctttgccc acatagtcat 120

ttacctccac agccgtttgt tgtcatagaa ggggtggtgg tgtttggatt tgattttttt 180

caacttgcag tgagaaatag gataggtgac aaaaccttac ttgttttctt aagacaattc 240

agtgcttgag catctctgtc agaaatggaa tgaaatactg ttagccaatt agaattattt 300

tatgtattgt tattgtgttt tgctgatttt tatatgaaaa tataattatt cattcttgat 360

ctctggaagc aa 372

<210> 98
<211> 365
<212> DNA
<213> Homo Sapiens

<400> 98
gggagccaag gctttatacg tctaaagaaa atattcagta gctgaatccg cccagtgata 60

gcctgtgggc accagcagca agggctgcca tgggatacag cacccatcta caaagacctc 120

tattacataa acactgcttc ttacaggaaa caaacctctt ctgggatctc cttttgtgaa 180

aaccagtttg atgtgctaaa agtaaaaagt ctattttcca gtgtggtctt gttcagaagc 240

agccagattt ccaatgttgt ttttccccctc cactcagaaa cccctgccct ttcccttcag 300

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ctggg 365

<210> 99
<211> 465
<212> DNA
<213> Homo Sapiens

<220>
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<222> (110)..(110)
<223> n is a, c, g, or t

<400> 99
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ccttaaaagg gagtcttatg ttttcaacta cagatagttg taagggatcn tacagaagat 120

attgatgata gttgaaatat tcttagaagg ggtgtgtatg tctagctgtg tctaccatgt 180

gtatgtattc ttgacaagca gtataaaata cctgtgattt ttctttacat tagggataat 240

gcataaggaa ttaatcttca tatatattat catccctaat gtagcagggg gaagtattta 300

attgcccatg atatgtattt tacttatact atgccagaga ggaaactata aagtaattac 360

acatgtaatc ttgggttttt cacatatgta ggtattcatt ttgagtaggt tgaagaagaa 420

aaaaaatatt taaatgaatt gaattcctga tgggatagta tcaat 465

<210> 100
<211> 515
<212> DNA
<213> Homo Sapiens

<400> 100
gaactctgca tcttcatggt ttacagaaat tggtgcaggc agccagcagt tagattccat 60

tcatgtaaca cagttggaga gagataccgt tttagtgtgt ttagacaaat ttgtgaaaat 120

tgtaaatcta caaggaaaat taaaatcaag taagaaactg gcctctgagt taagttttga 180

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ttttcgcatt gaatctgtag tatgccttca agacagtgtg ttggctttct ggaaacatgg    240

gatgcagggt aaaagcttca agtcagatga ggttacccag gagatttcag atgaaacaag    300

agttttccgc ttattaggat cagacagggt tgtcgttttg gaaagtaggc caacagaaaa    360

tcctactgca cacagcaatc tctacatctt ggctggacat gaaaatagtt actaagcaac    420

agaaactgat ctcaaatgac aggaaaatga atatactcca ttgaaaggga aaataaggaa    480

attcaataca aactgcacta tgatttgctt taact                               515
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<210>  101
<211>  525
<212>  DNA
<213>  Homo Sapiens

<400>  101
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cctggtgctg ccacacttca ggctcttctc ctttcacaac cttctgtggc tcacagaacc    120

cttggagcca atggagactg tctcaagagg gcactggtgg cccgacagcc tggcacaggg    180

cagtgggaca gggcatggcc aggtggccac tccagacccc tggcttttca ctgctggctg    240

ccttagaacc tttcttacat tagcagtttg ctttgtatgc actttgtttt tttctttggg    300

tcttgttttt tttttccact tagaaattgc atttcctgac agaaggactc aggttgtctg    360

aagtcactgc acagtgcatc tcagcccaca tagtgatggt tcccctgttc actctactta    420

gcatgtccct accgagtctc ttctccactg gatggaggaa aaccaagccg tggcttcccg    480

ctcagccctc cctgcccctc ccttcaacca ttccccatgg gaaat                    525
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<210>  102
<211>  418
<212>  DNA
<213>  Homo Sapiens

<400>  102
gcaacaaccg aaaatgcacc agccccaggt cctcggacac cgaggagaat gtcaagaggc     60

gaacacacaa cgtcttggag cgccagagga ggaacgagct aaaacggagc tttttttgccc   120

tgcgtgacca gatcccggag ttggaaaaca atgaaaaggc ccccaaggta gttatcctta    180

aaaaagccac agcatacatc ctgtccgtcc aagcagagga gcaaaagctc atttctgaag    240

aggacttgtt gcggaaacga cgagaacagt tgaaacacaa acttgaacag ctacggaact    300

cttgtgcgta aggaaaagta aggaaaacga ttccttctaa cagaaatgtc ctgagcaatc    360

acctatgaac ttgtttcaaa tgcatgatca aatgcaacct cacaaccttg gctgagtc      418
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<210>  103
<211>  462
<212>  DNA
<213>  Homo Sapiens

<400>  103
aacatccgcc tggtaaccag tcgctctggc tgggcacttc cacccgcacc tcattcctac     60

atcaatgagt ggctccaaat agacctgggg gaggagaaga tcgtgagggg catcatcatt    120

cagggtggga agcaccgaga gaacaaggtg ttcatgagga agttcaagat cgggtacagc    180

aacaacggct cggactggaa gatgatcatg gatgacagca aacgcaaggc gaagtctttt    240
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gagggcaaca acaactatga tacacctgag ctgcggactt ttccagctct ctccacgcga 300

ttcatcagga tctaccccga gagagccact catggcggac tggggctcag aatggagctg 360

ctgggctgtg aagtggaagc ccctacagct ggaccgacca ctcccaacgg gaacttggtg 420

gatgaatgtg atgacgacca ggccaactgc cacagtggaa ca 462

<210> 104
<211> 370
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (168)..(168)
<223> n is a, c, g, or t

<400> 104
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gatttttatc atgccatgtt ggacatgaga ttttttagat cttccttccc acattgctag 120

acgtctcact caaagacatt tgttgggagt cacatttgca tcataganga gacagtccat 180

tcatcttagt taaattggat tgagaatgcc ttttgtttcc aggaaaatat tgatcaccat 240

gaaagaagaa tagtttttttg tccccagaga cattcattta gttgatataa tcctaccaga 300

aggaaagcac taagaaacac tcgtttgttg tttttaaagg caacagactt aaagttgtcc 360

tcagccaagg 370

<210> 105
<211> 434
<212> DNA
<213> Homo Sapiens

<400> 105
caggtgtatc tgcacagtgg tcgccccaca gcagaccatg tgttcacggg atgcccgcac 60

aaaacagctg aggcagctac tggagaaggt gcagaacatg tctcaatcca tagaggtctt 120

ggacaggcgg acccagagag acttgcagta cgtggagaag atggagaacc aaatgaaagg 180

actggagtcc aagttcaaac aggtggagga gagtcataag caacacctgg ccaggcagtt 240

taagggctaa cttaaaagag ttttttcaat gctgcagtga ctgaagaagc agtccactcc 300

catgtaacca tgaaagagag ccagagagct ttttgcacca tgcattttta ctattatttt 360

ccaatactta gcaccatttc actaaggaac cttgaataca accaggatcc tcctttgcat 420

gcgactgtag ctgc 434

<210> 106
<211> 503
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (158)..(158)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (216)..(217)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (231)..(231)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (250)..(250)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (261)..(261)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (291)..(291)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (297)..(297)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (341)..(341)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (352)..(352)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (365)..(365)
<223> n is a, c, g, or t

<400> 106
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ccccggtttt cctccccgcc ctgtccctct ctggtcaaac aacatactaa agaggcgagg 120

caatgactgt tggccagttc tcaccgggga aaaacccnac tgttaggatg gcatgaacat 180

ttccttagat cgtggtcagc tccgaggaat gtggcnncca ggctctttga ngagccatgg 240

gctgcacccn ggccgtaggc ntagtgtaac tcgcatccca ttgcagtgcc ngtttcnttg 300

actgtgttgc tgtctcttag attaaccgtg ctgaggctcc nacatagctc cntggacctg 360

tgtcntagta catactgaag cgatggtcag agtgtgtaga gtgaagttgc tgtgcccaca 420

ttgtttgaac tcgcgtaccc cgtagataca ttgtgcaacg ttcttctgtt attcccttga 480

ggtggtaact tcgtatgttc agt 503

<210> 107
<211> 556
<212> DNA
<213> Homo Sapiens

<400> 107
ggagacttga gcttgaccta aggatatgca ttaaccactc tacagactcc cactcagtac 60

tgtacagggt ggctgtggtc ctagaagttc agtttttact gaggaaatat ttccattaac 120

agcaattatt atattgaagg ctttaataaa ggccacagga gacattacta tagcatagat 180

tgtcaaatgt aaatttactg agcgtgtttt ataaaaaact cacaggtgtt tgaggccaaa 240

acagatttta gacttacctt gaacggataa gaatctatag ttcactgaca cagtaaaatt 300

aactctgtgg gtgggggcgg ggggcatagc tctaatctaa tatataaaat gtgtgatgaa 360

tcaacaagat ttccacaatt cttctgtcaa gcttactaca gtgaaagaat gggattggca 420

agtaacttct gacttactgt cagttgtact tctgctccat agacatcagt attctgccat 480

catttttgat gactacctca gaacataaaa aggaacgtat atcacataat tccagtcaca 540

gtttttggtt cctctt 556

<210> 108
<211> 543
<212> DNA
<213> Homo Sapiens

<400> 108
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atagaaagta acaaaatttg ctgtcacctt aaataagaca ttttaatttt gttataatgt 120

acaatttaga agtttgatta attatattat ctatttaggc attaatataa aagaggtagg 180

agtctgttat ttaaaaaaag cattaaattt aaaaaaaaac tgtcttgtct acttttagct 240

tcattctccc atattttgaa gggtgtgtaa cttcagctct gcaggattgc atggggtaaa 300

acttgttacc aacacatgtg aaccattgct acattgtagg ttgtgatcat tttgccccac 360

tgaagcccat gtatctgacc ttacgtgcct tttgaactag gagaatcggg ctaatttatt 420

aatgatgata attataatgt atctgtacag cactttttac atttgcgaag tgctttccaa 480

tccatgttag ttactagtta ttacagctgt aaggataaaa cacgtcatgt ggattcattt 540

tga 543

<210> 109
<211> 458
<212> DNA
<213> Homo Sapiens

<400> 109
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gaaacactat ttgtgacttt ttaaacgatt agtgatgtcc ttaaaatgtg gtctgccaat 120

ctgtacaaaa tggtcctatt tttgtgaaga gggacataag ataaaatgat gttatacatc 180

aatatgtata tatgtatttc tatatagact tggagaatac tgccaaaaca tttatgacaa 240

gctgtatcac tgccttcgtt tatatttttt taactgtgat aatccccaca ggcacattaa 300

ctgttgcact tttgaatgtc caaaatttat attttagaaa taataaaaag aaagatactt 360

acatgttccc aaaacaatgg tgtggtgaat gtgtgagaaa aactaacttg atagggtcta 420

ccaatacaaa atgtattacg aatgcccctg ttcatgtt 458

<210> 110
<211> 412
<212> DNA

<213> Homo Sapiens

<400> 110
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gatagctgtt tctgggtatt taataggaat cctttctcaa ggaatgagtt gtgacctgtt 180

tactgtctct ttagaagaaa aactccactg gaaaccattc accatgtgtg actgtcttct 240

gttatcattt gtcttacagg cggctattgc agacggctaa tttatgctta acttaggaag 300

agataaggca agagctagat ttttttcatg tgatcttttc caagcttcaa cttaacttaa 360

ctacatttct ctgtatgatg atgtctctta cttctacagg ttccttgagc ac 412

<210> 111
<211> 514
<212> DNA
<213> Homo Sapiens

<400> 111
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tgtgggagta aaactttaat gggaggggag ggctggctgc tggaagaagg aagaagccag 120

actggttaga cagtactctt aactcctagc ccagcctacg tgccctgccc ctctggccac 180

tgctgcagac acctgcctta acacacacac ctctaggact ccacagtttt gccttaaagg 240

accttcccaa gtctcccttt ccctgtctgg cttctccctt aagaagagag agatacttgt 300

agaattgggt gggggaatg agcatgaact gtccttccat ttgggatatg ttacattaga 360

gtgagagaga gaataaggag cctttcttat ggaagaaatg ggagaagaga gacagggttc 420

ttttcagcag agtctagtag tttctctgta aggcaaaata atctaaaaag actaacctgc 480

ccacccactc cttatattgc tgtgagattg cccc 514

<210> 112
<211> 489
<212> DNA
<213> Homo Sapiens

<400> 112
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attttaggat ttgacttttt cactaaccag ttgacgagca gtgcatttac aaggcactgc 120

caaacaagat gcccttggga gctgtgaggg aaagaggacc tgcgggctta gatcaatctc 180

aattcctttt catgccctcc tgcattgctg ctgcgtgggt atttgtctcc ttagccatca 240

ggtacagttt acactacaat gtaagctata ggtggagcat cagcagtgag tgaggccatt 300

cttcatcctt aggatgtggc aatgaaatga tggtgcaagt tcctttctct tttgtgaatc 360

tttcccccca tttcctgttt acatgtaacc caacaaaatg caatttctag tgccttctgt 420

ccaatcagtt ctttcctctg agtgagacgt acttggctac agatttctgc cttgttttgc 480

gacattgtc 489

<210> 113
<211> 416
<212> DNA
<213> Homo Sapiens

<400> 113
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tcttgatcgt ggtggtgttc ctcatcgctg ggacgctggt tctagaggca gctgtcacgg 120

gagttcctgt taaaggtcaa gacactgtca aaggccgtgt tccattcaat ggacaagatc 180

ccgttaaagg acaagtttca gttaaaggtc aagataaagt caaagcgcaa gagccagtca 240

aaggtccagt ctccactaag cctggctcct gccccattat cttgatccgg tgcgccatgt 300

tgaatccccc taaccgctgc ttgaaagata ctgactgccc aggaatcaag aagtgctgtg 360

aaggctcttg cgggatggcc tgtttcgttc cccagtgaag ggagccggtc cttgct 416

<210> 114
<211> 502
<212> DNA
<213> Homo Sapiens

<400> 114
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agtgtaagca gctgaggtct cttgagggag cttagccaat gtgggagcag cggtttgggg 120

agcagagaca ctaacgactt cagggcaggg ctctgatatt ccatgaatgt atcaggaaat 180

atatatgtgt gtgtatgttt gcacacttgt tgtgtgggct gtgagtgtaa gtgtgagtaa 240

gagctggtgt ctgattgtta agtctaaata tttccttaaa ctgtgtggac tgtgatgcca 300

cacagagtgg tctttctgga gaggttatag gtcactcctg ggcctcttgg ggtcccccac 360

gtgacagtgc ctgggaatgt acttattctg cagcatgacc tgtgaccagc actgtctcag 420

tttcactttc acatagatgt ccctttcttg gccagttatc ccttcctttt agcctagttc 480

atccaatcct cactgggtgg gg 502

<210> 115
<211> 430
<212> DNA
<213> Homo Sapiens

<400> 115
accacaacga cattgccttg ctgaagatcc gttccaagga gggcaggtgt gcgcagccat 60

cccggactat acagaccatc tgcctgccct cgatgtataa cgatccccag tttggcacaa 120

gctgtgagat cactggcttt ggaaaagaga attctaccga ctatctctat ccggagcagc 180

tgaagatgac tgttgtgaag ctgatttccc accgggagtg tcagcagccc cactactacg 240

gctctgaagt caccaccaaa atgctgtgtg ctgctgaccc acagtggaaa acagattcct 300

gccagggaga ctcaggggga cccctcgtct gttccctcca aggccgcatg actttgactg 360

gaattgtgag ctggggccgt ggatgtgccc tgaaggacaa gccaggcgtc tacacgagag 420

tctcacactt 430

<210> 116
<211> 449
<212> DNA
<213> Homo Sapiens

<400> 116
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ggactctaat acctgtttaa tattgtcttc ctaattggga taatttaatt aacaagattg 120

actagaagtg aaactgcaac actaacttcc ccgtgctgtg gtgtgacctg agttggtgac 180

acaggccaca gaccccagag cttggctttt gaaacacaac tcagggcttt tgtgaaggtt 240

cccccgctga gatctttcct cctggttact gtgaagcctg ttggtttgct gctgtcgttt 300

ttgaggaggg cccatggggg taggagcagt tgaacctggg aacaaacctc acttgagctg 360

tgcctagaca atgtgaattc ctgtgttgct aacagaagtg gcctgtaagc tcctgtgctc 420

cggagggaag catttcctgg taggctttg 449

<210> 117
<211> 535
<212> DNA
<213> Homo Sapiens

<400> 117
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gaagggcttc ggctacaaag gctccacctt ccacagggtg atcccttcct tcatgtgcca 120

ggcgggcgac ttcaccaacc acaatggcac aggcgggaag tccatctacg gaagccgctt 180

tcctgacgag aactttacac tgaagcacgt ggggccaggt gtcctgtcca tggctaatgc 240

tggtcctaac accaacggct cccagttctt catctgcacc ataaagacag actggttgga 300

tggcaagcat gttgtgttcg gtcacgtcaa agagggcatg gacgtcgtga agaaaataga 360

atctttcggc tctaagagtg ggaggacatc caagaagatt gtcatcacag actgtggcca 420

gttgagctaa tctgtggcca gggtgctggc atggtggcag ctgcaaatgt ccatgcaccc 480

aggtggccgc gttgggctgt cagccaaggt gcctgaaacg atacgtgtgc ccact 535

<210> 118
<211> 484
<212> DNA
<213> Homo Sapiens

<400> 118
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tagcctgaat gtgccataag actgaccttt taaaatgttt tgagggatct gtggatgctt 120

cgttaatttg ttcagccaca atttattgag aaaatattct gtgtcaagca ctgtgggttt 180

taatattttt aaatcaaacg ctgattacag ataatagtat ttatataaat aattgaaaaa 240

aattttcttt tgggaagagg gagaaaatga aataaatatc attaaagata actcaggaga 300

atcttcttta caattttacg tttagaatgt ttaaggttaa gaaagaaata gtcaatatgc 360

ttgtataaaa cactgttcac tgtttttttt aaaaaaaaaa cttgatttgt tattaacatt 420

gatctgctga caaaacctgg gaatttgggt tgtgtatgcg aatgtttcag tgcctcagac 480

aaat 484

<210> 119
<211> 495
<212> DNA
<213> Homo Sapiens

<400> 119

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attccttgat ttaaagaaga acacaggaaa ggaagagcag cgtgccagag atcttttctt 120

tgctctttgg attccggatc tcttcatgaa acgagtggag actaatcagg actggtcttt 180

gatgtgtcca aatgagtgtc ctggtctgga tgaggtttgg ggagaggaat ttgagaaact 240

atatgcaagt tatgagaaac aaggtcgtgt ccgcaaagtt gtaaaagctc agcagctttg 300

gtatgccatc attgagtctc agacggaaac aggcaccccg tatatgctct acaaagattc 360

ctgtaatcga aagagcaacc agcagaacct gggaaccatc aaatgcagca acctgtgcac 420

agaaatagtg gagtacacca gcaaagatga ggttgctgtt tgtaatttgg cttccctggc 480

cctgaatatg tatgt 495

<210> 120
<211> 438
<212> DNA
<213> Homo Sapiens

<400> 120
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tgagcggggg ccgcgcagcg caacgcactg gtgaccagac tgtccccacg ccgggaacca 120

agcaggagac gacaggcgag agaggagcca gacagaccct gaaaagaagg acgggttggg 180

gccgggcaca ttgggggtca ccggccgatg gagacaccaa ccgacaggcc ctggctgagg 240

gcagctgcgc gggcttattt attaacagga taacccttga atgtagcagc cccgggaggg 300

cggcacaggt cgggcgcagg attcagccgg agggaaggga cggggaagcc gagctccaga 360

gcaacgacca gggccgagga ggtgcctgga gtgcccaccc tgggagacag accccacctc 420

cttgggtagt gagcagtg 438

<210> 121
<211> 447
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (116)..(116)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (362)..(362)
<223> n is a, c, g, or t

<400> 121
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acattgccat cactcttgta ctgcctgcca ccgcggagga ggctggtgac aggccnaaag 120

gccagtggaa gaaacaccct ttcatctcag agtccactgt ggcactggcc acccctcccc 180

agtacagggg tgctgcaggt ggcagagtga atgtccccca tcatgtggcc caactctcct 240

ggcctggcca tctccctccc cagaaacagt gtgcatgggt tattttggag tgtaggtgac 300

ttgtttactc attgaagcag atttctgctt ccttttattt ttataggaat agaggaagaa 360

angtcagatg cgtgcccagc tcttcacccc ccaatctctt ggtggggagg ggtgtaccta 420

aatatttatc atatccttgc ccttgag 447

<210> 122
<211> 323
<212> DNA
<213> Homo Sapiens

<400> 122
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agactcagat gaggacagag tggtttccaa tgtgttcaat agatttagga gcagaaatgc 120

aaggggctgc atgacctacc aggacagaac tttccccaat tacagggtga ctcacagccg 180

cattggtgac tcacttcaat gtgtcatttc cggctgctgt gtgtgagcag tggacacgtg 240

agggggggt gggtgagaga gacaggcagc tcggattcaa ctaccttaga taatatttct 300

gaaaacctac cagccagagg gta 323

<210> 123
<211> 499
<212> DNA
<213> Homo Sapiens

<400> 123
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ttttcttttt tttaaaccat gaagagccgt ttgacagagc atgctctgcg ttgttggttt 120

caccagcttc tgccctcaca tgcacaggga tttaacaaca aaaatataac tacaacttcc 180

cttgtagtct cttatataag tagagtcctt ggtactctgc cctcctgtca gtagtggcag 240

gatctattgg catattcggg agcttcttag agggatgagg ttctttgaac acagtgaaaa 300

tttaaattag taactttttt gcaagcagtt tattgactgt tattgctaag aagaagtaag 360

aaagaaaaag cctgttggca atcttggtta tttctttaag atttctggca gtgtgggatg 420

gatgaatgaa gtggaatgtg aactttgggc aagttaaatg ggacagcctt ccatgttcat 480

ttgtctacct cttaactga 499

<210> 124
<211> 328
<212> DNA
<213> Homo Sapiens

<400> 124
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tgcccatctt cactctagcc ttcgtatttg tgaaggactc agccaccttc cttcttcacc 120

ccatgcttct caccaaattt ttgttgtcat tgagggcact tggataactc aagttgatat 180

ttatagctga tcaatctata tgtgtcacag aactatgctg cctaaagtga tcttggctcc 240

ttaatggtcc ttttggcccc ttggatagtt aacagctgag taattctaat ctcttctgtg 300

ttttccttgc cttaaccaca aattgtgg 328

<210> 125
<211> 489
<212> DNA
<213> Homo Sapiens

<400> 125
gagatacaga acttggtgac ccatgtattg cataagctaa agcaacacag acactcctag 60

gcaaagtttt tgtttgtgaa tagtacttgc aaaacttgta aattagcaga tgactttttt 120

ccattgtttt ctccagagag aatgtgctat atttttgtat atacaataat atttgcaact 180

gtgaaaaaca agttgtgcca tactacatgg cacagacaca aaatattata ctaatatgtt 240

gtacattcgg aagaatgtga atcaatcagt atgtttttag attgtatttt gccttacaga 300

aagcctttat tgtaagactc tgatttccct ttggacttca tgtatattgt acagttacag 360

taaaattcaa cctttatttt ctaatttttt caacatattg tttagtgtaa agaatattta 420

tttgaagttt tattatttta taaaaaagaa tatttatttt aagaggcatc ttacaaattt 480

tgccccttt 489

<210> 126
<211> 503
<212> DNA
<213> Homo Sapiens

<400> 126
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ggagcaacag ctgtcagcca acatcatcga ggagctcagg caatttcagc gcctcactcg 120

ctcctacttc aacatggtgt tgattgacaa gcagggtatt gaccgagacc gctacatgga 180

acctgtcacc cccgaggaaa tcttcacatt cattgatgac tacctactga gcaatcagga 240

gttgacccag cgtcgggagc aaagggacat atgcgagtga acttgagcca gggcatggtt 300

aaagtcaagg gaaaagctcc tctagttagc tgaaactggg acctaataaa aggaggaaat 360

gttttcccac agttctaggg acaggactct gaggtgggtg agtttgacaa atcctgcagt 420

gtttccaggc atccttttag gactgtgtaa tagtttccct agaagctagg tagggactga 480

ggacaggcct tgggcagtgg gtt 503

<210> 127
<211> 436
<212> DNA
<213> Homo Sapiens

<400> 127
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aagtctcctg ttcgctcata aagaagtttt tgggatggga gagaatccag accatcttgg 120

ggcagccagg cccttgcctt catttttaca gaggtagcac aactgattcc aacacaaaac 180

cccttcccct ttttaaaatg atttctgttc taatgccata gatcaaaggc ctcagaaacc 240

attgtgtgtt tcctctttga agcaatgaca agcactttac tttcacggtg gtttttgttt 300

tttcttattg ctgtggaacc tcttttggag gacgttaaag gcgtgtttta cttgtttttt 360

taagagtgtg tgatgtgtgt tttgtagatt tcttgacagt gctgtaatac agacggcaat 420

gcaatagcct atttaa 436

<210> 128
<211> 497
<212> DNA
<213> Homo Sapiens

<400> 128
cctgccctct agttggttct gggctttgat ctcttccaac ctgcccagtc acagaaggag 60

gaatgactca aatgcccaaa accaagaaca cattgcagaa gtaagacaaa catgtatatt 120

tttaaatgtt ctaacataag acctgttctc tctagccatt gatttaccag gctttctgaa 180

agatctagtg gttcacacag agagagagag agtactgaaa aagcaactcc tcttcttagt 240

cttaataatt tactaaaatg gtcaactttt cattatcttt attataataa acctgatgct 300

ttttttaga actccttact ctgatgtctg tatatgttgc actgaaaagg ttaatattta 360

atgttttaat ttattttgtg tggtaagtta attttgattt ctgtaatgtg ttaatgtgat 420

tagcagttat tttccttaat atctgaatta tacttaaaga gtagtgagca atataagacg 480

caattgtgtt tttcagt 497

<210> 129
<211> 321
<212> DNA
<213> Homo Sapiens

<400> 129
gtttggatgg tggaaggtct cattttattg agatttttaa gatacatgca aaggtttgga 60

aatagaacct ctaggcaccc tcctcagtgt gggtgggctg agagttaaag acagtgtggc 120

tgcagtagca tagaggcgcc tagaaattcc acttgcaccg tagggcatgc tgataccatc 180

ccaatagctg ttgcccattg acctctagtg gtgagtttct agaatactgg tccattcatg 240

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tgtcagagga tactgtggct t 321

<210> 130
<211> 553
<212> DNA
<213> Homo Sapiens

<400> 130
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ctaagataca ctgcactttg tttagaaaaa aaactgaaga tgaaatatat attgtaaaga 120

agggatatta agaatcttag ataacttctt gaaaaagatg gcttatgtca tcagtaaagt 180

acctttatgt tatgaggata taatgtgtgc tttattgaat tagaaaatta gtgaccatta 240

ttcacaggtg gacaaatgtt gtcctgttaa tttataggag ttttttgggg atgtggaggt 300

agttgggtag aaaaattatt agaacattca cttttgttaa cagtatttct cttttattct 360

gttatatagt ggatgatata cacagtggca aaacaaaagt acattgctta aaatatatag 420

tgaaaaatgt cactatatct tcccatttaa cattgttttt gtatattggg tgtagatttc 480

tgacatcaaa acttggaccc ttggaaaaca aaagttttaa ttaaaaaaaa tccttgtgac 540

ttacaatttg cac 553

<210> 131
<211> 419
<212> DNA
<213> Homo Sapiens

<400> 131
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gatgttcctg agtctggagc aagcacccag gccagaataa cagagctttc ttagttggtg 120

aagacttaaa catctgcctg aggtcaggag gcaatttgcc tgccttgtac aaaagctcag 180

gtgaaagact gagatgaatg tctttcctct ccctgcctcc caccagactt cctcctggaa 240

aacgctttgg tagatttggc caggagcttt cttttatgta aattggataa atacacacac 300

catacactat ccacagatat agccaagtag atttgggtag aggatactat ttccagaata 360

gtgtttagct cacctagggg gatatgtttg tatacacatt tgcatatacc cacatgggg 419

<210> 132
<211> 414
<212> DNA
<213> Homo Sapiens

<400> 132
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ttttaattaa aatttgaaat tctgaacacc gtcagcaccc tctcttccct atcatgggtc 120

atctgacccc tgtccgtctc cttgtccctg cttcatgttt gggggccttt ctttaactgc 180

cttcctggct tagctcagat ggcagatgag agtgtagtca agggcctggg cacaggaggg 240

agagctgcag agtgtcctgc ctgccttggc tggagggaca cctctcctgg gtgtggagac 300

agcttggttc cctttcccta gctccctggt gggtgaatgc cacctcctga gatcctcacc 360

tcttggaatt aaaattgttg gtcactgggg aaagcctgag tttgcaacca gttg 414

<210> 133
<211> 419
<212> DNA
<213> Homo Sapiens

<400> 133
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tgccttgctt tgtgacttcc aagaacgagt gtctctggac cgacatgctc tccaatttcg 120

gttaccctgg ctaccagtcc aaacactacg cctgcatccg gcagaagggc ggctactgca 180

gctggtaccg aggatgggcc cccccggata aaagcatcat caatgccaca gacccctgag 240

cgccagaccc tgccccacct cacttccctc ccttcccgct gagcttccct tggacactaa 300

ctcttcccag atgatgacaa tgaaattagt gcctgttttc ttgcaaattt agcacttgga 360

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<210> 134
<211> 493
<212> DNA
<213> Homo Sapiens

<400> 134
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atgccccaga cctctgtctt gcatgtgaca attgacaatc tggactaccc caagatggca 120

cccaagtgtt tggcttctgg ctacctaagg ttaacatgtc actagagtat ttttatgaga 180

gacaaacatt ataaaaatct gatggcaaaa gcaaaacaaa atggaaagta ggggaggtgg 240

atgtgacaac aacttccaaa ttggctcttt ggaggcgaga ggaaggggag aacttggaga 300

atagtttttg ctttgggggt agaggcttct tagattctcc cagcatccgc ctttcccttt 360

agccagtctg ctgtcctgaa acccagaagt gatggagaga aaccaacaag agatctcgaa 420

ccctgtctag aaggaatgta tttgttgcta aatttcgtag cactgtttac agttttcctc 480

catgttattt atg 493

<210> 135
<211> 567
<212> DNA
<213> Homo Sapiens

<400> 135
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gactgccctt agaaattcta gcctggtttg gagatactaa ctgctctcag agaaagtagc 180

tttgtgacat gtcatgaacc catgtttgca atcaaagatg ataaaataga ttcttatttt 240

tcccccaccc ccgaaaatgt tcaataatgt cccatgtaaa acctgctaca aatggcagct 300

tatacatagc aatggtaaaa tcatcatctg gatttaggaa ttgctcttgt catacccccca 360

agtttctaag atttaagatt ctccttacta ctatcctacg tttaaatatc tttgaaagtt 420

tgtattaaat gtgaatttta agaaataata tttatatttc tgtaaatgta aactgtgaag 480

atagttataa actgaagcag atacctggaa ccacctaaag aacttccatt tatggaggat 540

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<210> 136
<211> 479
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (441)..(441)
<223> n is a, c, g, or t

<400> 136
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atgttgactt gagtaaatat atcaccacta ttgctggagt catgacacta agtcaagtta 120

aaggctttgt tcgaaagaat ggtgtcaatg aagccaaaat agatgagatc aagaatgaca 180

atgtccaaga cacagcagaa cagaaagttc aactgcttcg taattggcat caacttcatg 240

gaaagaaaga agcgtatgac acattgatta aagatctcaa aaaagccaat ctttgtactc 300

ttgcagagaa aattcagact atcatcctca aggacattac tagtgactca gaaaattcaa 360

acttcagaaa tgaaatccaa agcttggtct agagtgaaaa acaacaaatt cagttctgag 420

tatatgcaat tagtgtttga naagattctt aatagctggc tgtaaatact gcttggttt 479

<210> 137
<211> 490
<212> DNA
<213> Homo Sapiens

<400> 137
gtagcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc 60

aagaatgaaa aggctctggg ccgcaaaata aactcctggg aatcatcaag gagtgggcat 120

tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt 180

tactacatct attcccaaac atactttcga tttcaggagg aaataaaaga aaacacaaag 240

aacgacaaac aaatggtcca atatatttac aaatacacaa gttatcctga ccctatattg 300

ttgatgaaaa gtgctagaaa tagttgttgg tctaaagatg cagaatatgg actctattcc 360

atctatcaag gggaatatt tgagcttaag gaaaatgaca gaatttttgt ttctgtaaca 420

aatgagcact tgatagacat ggaccatgaa gccagttttt tcggggcctt tttagttggc 480

taactgacct 490

<210> 138
<211> 248
<212> DNA
<213> Homo Sapiens

<400> 138
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tgcaatggtt aacatcttct gtctttataa tctactcctt gtaaagactg tagaagaaag 120

cgcaacaatc catctctcaa gtagtgtatc acagtagtag cctccaggtt tccttaaggg 180

acaacatcct taagtcaaaa gagagaagag gcaccactaa aagatcgcag tttgcctggt 240

gcagtggc 248

<210> 139
<211> 405
<212> DNA
<213> Homo Sapiens

<220>
<221> misc_feature
<222> (64)..(64)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (68)..(68)
<223> n is a, c, g, or t

<400> 139
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ccgnctanct gacggtggcc accgtgttcc ggggccgcat gtccatgaag gaggtggacg 120

agcagatgct ggccatccag agcaagaaca gcagctactt cgtggagtgg atccccaaca 180

acgtgaaggt ggccgtgtgt gacatcccgc cccgcggcct caagatgtcc tccaccttca 240

tcgggaacag cacggccatc caggagctgt tcaagcgcat ctccgagcag ttcacggcca 300

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tcaccgaggc cgagagcaac atgaacgacc tggtgtccga gtacc 405

<210> 140
<211> 407
<212> DNA

<213> Homo Sapiens

<400> 140
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aaagcagtgt gcttcaaagg catcagacga tgaaagcaac ataccacaac taggagttat 120

ttctcaaact taaatgtcct ctgggaatcc agacttaaaa ataagagcaa acttaacaca 180

ctatccattt tcgagcaaac ttaacccact atatccattt tgctcatgtg ttttatgcaa 240

ccagctttcc atcaaatcct caatccttga atccaggtaa aaggttaatt atcctaggat 300

tagtgaatga ttcaatgaag ctttcttgaa aacaaacata ggagtgtaat gtactattat 360

gtttgtatcc tgttttagtt tataaagcac tttcacatac attatgg 407

<210> 141
<211> 518
<212> DNA
<213> Homo Sapiens

<400> 141
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ttatttgaga aggaacaact tggagttcat ctataacaag actggttggg ccatggtgtc 120

tctgtgtata gtctttgcta tgacttctgg ccagatgtgg aaccatatcc gtggacctcc 180

atatgctcat aagaacccac acaatggaca agtgagctac attcatggga gcagccaggc 240

tcagtttgtg gcagaatcac acattattct ggtactgaat gccgctatca ccatggggat 300

ggttcttcta aatgaagcag caacttcgaa aggcgatgtt ggaaaaagac ggataatttg 360

cctagtggga ttgggcctgg tggtcttctt cttcagtttt ctactttcaa tatttcgttc 420

caagtaccac ggctatcctt atagtgatct ggactttgag tgagaagatg tgatttggac 480

catggcactt aaaaactcta taacctcagc cttttaat 518

<210> 142
<211> 443
<212> DNA
<213> Homo Sapiens

<400> 142
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gaacccacac aatggacaag tgagctacat tcatgggagc agccaggctc agtttgtggc 120

agaatcacac attattctgg tactgaatgc cgctatcacc atggggatgg ttcttctaaa 180

tgaagcagca acttcgaaag gcgatgttgg aaaaagacgg ataatttgcc tagtgggatt 240

gggcctggtg gtcttcttct tcagttttct actttcaata tttcgttcca agtaccacgg 300

ctatccttat agctttttaa ttaaatgaag ccaagtggga tttgcataaa gtgaatgttt 360

accatgaaga taaactgttc ctgactttat actattttga attcattcat ttcattgtga 420

tcagctagct tattcttgtg tac 443